

# Sequence Listing

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Kljavin, Ivar J.  
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Pan, James  
Paoni, Nicholas F.  
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Zhang, Zemin
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Arg Ile Ile Gln Glu Arg Asn Gly Val Leu Pro Asp Cys Leu Thr	155	160	165
Asp Gly Ser Asp Val Val Ser Asp Leu Glu His Glu Glu Met Lys	170	175	180
Ile Leu Arg Glu Val Leu Arg Lys Ser Lys Glu Glu Tyr Asp Gln	185	190	195
Glu Glu Glu Arg Lys Arg Lys Lys Gln Leu Ser Glu Ala Lys Thr	200	205	210
Glu Glu Pro Thr Val His Ser Ser Glu Ala Ala Ile Met Asn Asn	215	220	225
Ser Gln Gly Asp Gly Glu His Phe Ala His Pro Pro Ser Glu Val	230	235	240
Lys Met His Phe Ala Asn Gln Ser Ile Glu Pro Leu Gly Arg Lys	245	250	255
Val Glu Arg Ser Glu Thr Ser Ser Leu Pro Gln Lys Gly Leu Lys	260	265	270
Ile Pro Gly Leu Glu His Ala Ser Ile Glu Gly Pro Ile Ala Asn	275	280	285
Leu Ser Val Leu Gly Thr Glu Glu Leu Arg Gln Arg Glu His Tyr	290	295	300
Leu Lys Gln Lys Arg Asp Lys Leu Met Ser Met Arg Lys Asp Met	305	310	315
Arg Thr Lys Gln Ile Gln Asn Met Glu Gln Lys Gly Lys Pro Thr	320	325	330
Gly Glu Val Glu Glu Met Thr Glu Lys Pro Glu Met Thr Ala Glu	335	340	345
Glu Lys Gln Thr Leu Leu Lys Arg Arg Leu Leu Ala Glu Lys Leu	350	355	360
Lys Glu Glu Val Ile Asn Lys	365		

<210> 9  
 <211> 418  
 <212> DNA  
 <213> Homo sapiens

<400> 9  
 gggcacagca catgtgaagt ttttgatgat gaagaagaaa gcaaattgac 50  
 ctatacagag attcatcagg aatacaaaga actagttgaa aagctgtag 100  
 aaggttacct caaagaaatt ggaattaatg aagatcaatt tcaagaagca 150  
 tgcacttctc ctcttgcaaa gaccataca tcacaggcca tttttgcaac 200  
 ctgtgttggc agcagaagat ttactatct ttaaagcaat gatggtccag 250  
 aaaaacattg aaatgcagct gcaagccatt cgaataattc aagagagaaa 300

tggtgtatta cctgactgct taaccgatgg ctctgatgtg gtcagtgacc 350  
 ttgaacacga agagatgaaa atcctgaggg aagttcttag aaaatcaaaa 400  
 gaggaatatg accaggaa 418

<210> 10  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 10  
 ttgacctata cagagattca tc 22

<210> 11  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 11  
 ctaagaactt ccctcaggat ttt 23

<210> 12  
 <211> 40  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 12  
 atgaagatca atttcaagaa gcatgcactt ctcctcttgc 40

<210> 13  
 <211> 2886  
 <212> DNA  
 <213> Homo sapiens

<400> 13  
 gogtgggtttt tgttctgcaa taggcggctt agagggaggg gctttttcgc 50  
 ctatacctac tgtagcttct ccacgtatgg accctaaagg ctactgctgc 100  
 tactacgggg ctagacagtt actgtctcag ctctaggatg tgcgttcttc 150  
 cactagaagc tottctgagg gaggttaatta aaaaacagtg gaatggaaaa 200  
 acagtgctgt agtcatcctg taatatgctc cttgtcaaca atgtatacat 250  
 tcctgctagg tgccatattc attgctttta gctcaagtcg catcttacta 300  
 gtgaagtatt ctgccaatga agaaaacaag tatgattatc ttccaactac 350  
 tgtgaatgtg tgctcagaac tggatgaagct agttttctgt gtgcttgtgt 400  
 cattctgtgt tataaagaaa gatcatcaaa gtagaaattt gaaatatgct 450





cagacacaac atctcagaat ttttaattttt agaaattcat gggaaattgg 2100  
 atttttgtaa taatcttttg atgttttaaa cattgggttcc ctagtcacca 2150  
 tagttaccac ttgtatttta agtcatttaa acaagccacg gtggggcttt 2200  
 tttctcctca gtttgaggag aaaaatcttg atgtcattac tcctgaatta 2250  
 ttacattttg gagaataaga gggcatttta ttttattagt tactaattca 2300  
 agctgtgact attgtatatc tttccaagag ttgaaatgct ggcttcagaa 2350  
 tcataccaga ttgtcagtga agctgatgcc taggaacttt taaagggatc 2400  
 ctttcaaaag gatcacttag caaacacatg ttgactttta actgatgtat 2450  
 gaatattaat actctaaaaa tagaaagacc agtaatatat aagtcacttt 2500  
 acagtgtac ttcacactta aaagtgcag gtatttttca tggatatttg 2550  
 catgcagcca gttaactctc gtagatagag aagtcaggtg atagatgata 2600  
 ttaaaaatta gcaaacaaaa gtgacttgct caggggtcatg cagctgggtg 2650  
 atgatagaag agtgggcttt aactggcagg cctgtatggt tacagactac 2700  
 catactgtaa atatgagctt tatggtgtca ttctcagaaa cttatacatt 2750  
 tctgctctcc tttctcctaa gtttcatgca gatgaatata aggtaatata 2800  
 ctattatata attcatttgt gatatccaca ataatatgac tggcaagaat 2850  
 tgggtgaaat ttgtaattaa aataattatt aaacct 2886

<210> 14  
 <211> 424  
 <212> PRT  
 <213> Homo sapiens

<400> 14  
 Met Glu Lys Gln Cys Cys Ser His Pro Val Ile Cys Ser Leu Ser  
     1                    5                    10                    15  
 Thr Met Tyr Thr Phe Leu Leu Gly Ala Ile Phe Ile Ala Leu Ser  
                     20                    25                    30  
 Ser Ser Arg Ile Leu Leu Val Lys Tyr Ser Ala Asn Glu Glu Asn  
                     35                    40                    45  
 Lys Tyr Asp Tyr Leu Pro Thr Thr Val Asn Val Cys Ser Glu Leu  
                     50                    55                    60  
 Val Lys Leu Val Phe Cys Val Leu Val Ser Phe Cys Val Ile Lys  
                     65                    70                    75  
 Lys Asp His Gln Ser Arg Asn Leu Lys Tyr Ala Ser Trp Lys Glu  
                     80                    85                    90  
 Phe Ser Asp Phe Met Lys Trp Ser Ile Pro Ala Phe Leu Tyr Phe  
                     95                    100                    105  
 Leu Asp Asn Leu Ile Val Phe Tyr Val Leu Ser Tyr Leu Gln Pro  
                     110                    115                    120

Ala Met Ala Val	Ile Phe Ser Asn Phe	Ser Ile Ile Thr Thr	Ala
125		130	135
Leu Leu Phe Arg	Ile Val Leu Lys Arg	Arg Leu Asn Trp Ile	Gln
140		145	150
Trp Ala Ser Leu	Leu Thr Leu Phe Leu	Ser Ile Val Ala Leu	Thr
155		160	165
Ala Gly Thr Lys	Thr Leu Gln His Asn	Leu Ala Gly Arg Gly	Phe
170		175	180
His His Asp Ala	Phe Phe Ser Pro Ser	Asn Ser Cys Leu Leu	Phe
185		190	195
Arg Ser Glu Cys	Pro Arg Lys Asp Asn	Cys Thr Ala Lys Glu	Trp
200		205	210
Thr Phe Pro Glu	Ala Lys Trp Asn Thr	Thr Ala Arg Val Phe	Ser
215		220	225
His Ile Arg Leu	Gly Met Gly His Val	Leu Ile Ile Val Gln	Cys
230		235	240
Phe Ile Ser Ser	Met Ala Asn Ile Tyr	Asn Glu Lys Ile Leu	Lys
245		250	255
Glu Gly Asn Gln	Leu Thr Glu Ser Ile	Phe Ile Gln Asn Ser	Lys
260		265	270
Leu Tyr Phe Phe	Gly Ile Leu Phe Asn	Gly Leu Thr Leu Gly	Leu
275		280	285
Gln Arg Ser Asn	Arg Asp Gln Ile Lys	Asn Cys Gly Phe Phe	Tyr
290		295	300
Gly His Ser Ala	Phe Ser Val Ala Leu	Ile Phe Val Thr Ala	Phe
305		310	315
Gln Gly Leu Ser	Val Ala Phe Ile Leu	Lys Phe Leu Asp Asn	Met
320		325	330
Phe His Val Leu	Met Ala Gln Val Thr	Thr Val Ile Ile Thr	Thr
335		340	345
Val Ser Val Leu	Val Phe Asp Phe Arg	Pro Ser Leu Glu Phe	Phe
350		355	360
Leu Glu Ala Pro	Ser Val Leu Leu Ser	Ile Phe Ile Tyr Asn	Ala
365		370	375
Ser Lys Pro Gln	Val Pro Glu Tyr Ala	Pro Arg Gln Glu Arg	Ile
380		385	390
Arg Asp Leu Ser	Gly Asn Leu Trp Glu	Arg Ser Ser Gly Asp	Gly
395		400	405
Glu Glu Leu Glu	Arg Leu Thr Lys Pro	Lys Ser Asp Glu Ser	Asp
410		415	420
Glu Asp Thr Phe			

<210> 15  
<211> 755  
<212> DNA  
<213> Homo sapiens

<400> 15  
cgtgcctgcg caatgggtgt cgggtccgct ttttcccaat ccggacgtaa 50  
tcgtgggtttt tgttctgcaa taggcggcctt agagggaggg gctttttcgc 100  
ctatacctac tgtagcttct ccacgtatgg accctaaagg ctactgctgc 150  
tactacgggg ctagacagtt actgtctcag ctctaggatg tgcgttcttc 200  
cactagaagc tcttctgagg gaggttaatta aaaaacagtg gaatggaaaa 250  
acagtgctgt agtcatcctg taatatgctc cttgtcaaca atgtatacat 300  
tcctgctagg tgccatattc attgctttta gctcaagtcg catcttacta 350  
gtgaagtatt ctgccaatga agaaaacaag tatgattatc ttccaactac 400  
tgtgaatgtg tgctcagaac tggatgaagct agttttctgt gtgcttgtgt 450  
cattctgtgt tataaagaaa gatcatcaaa gtagaaattt gaaatatgct 500  
tcctggaagg aattctctga ttctcatgaag tgggtccattc ctgcctttct 550  
ttatttcctg gataacttga ttgtcttcta tgtcctgtcc tatcttcaac 600  
cagccatggc tgttatcttc tcaaatttta gcattataac aacagctctt 650  
ctattcagga tagtgctgaa gaggcgtcta aactggatcc agtgggcttc 700  
cctcctgact ttatttttgt ctattgtggc cttgactgcc gggactaaaa 750  
cttta 755

<210> 16  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 16  
ctatacctac tgtagcttct 20

<210> 17  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 17  
tcagagaatt ccttccagga 20

<210> 18  
<211> 40  
<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 18

acagtgtctgt agtcatcctg taatatgctc cttgtcaaca 40

<210> 19

<211> 2142

<212> DNA

<213> Homo sapiens

<400> 19

cggacgcgtg ggcggacgcg tgggaggacg cgtggggccg gcttggctag 50  
cgcgcgggcg ccttggctaa ggctgctacg aagcgagctt gggaggagca 100  
gcggcctgcg gggcagagga gcatcccgtc taccaggtcc caagcggcgt 150  
ggccccgcggg tcatggccaa aggagaaggc gccgagagcg gctccgcggc 200  
ggggctgcta cccaccagca tctccaaag cactgaacgc ccggcccagg 250  
tgaagaaaga accgaaaaag aagaaacaac agttgtctgt ttgcaacaag 300  
ctttgtctatg cacttggggg agccccctac caggtgacgg gctgtgccct 350  
gggtttcttc cttcagatct acctattgga tgtggctcag gtggggccctt 400  
tctctgcctc catcatcctg tttgtgggcc gagcctggga tgccatcaca 450  
gacccccctg tgggcctctg catcagcaaa tccccctgga cctgcctggg 500  
tcgccttatg ccctggatca tcttctccac gccctggcc gtcattgcct 550  
acttctcat ctggttcgtg cccgacttcc cacacggcca gacctattgg 600  
tacctgcttt tctattgcct ctttgaaca atggtcacgt gtttccatgt 650  
tccctactcg gctctcacca tggtcatcag caaccgagca gactgagcgg 700  
gattctgcc aagcctatcg gatgactgtg gaagtgtggt gcacagtgt 750  
gggcacggcg atccaggagc aaatcgtggg ccaagcagac acgccttggt 800  
tccaggactt caatagctct acagtagctt cacaagtgc caaccatata 850  
catggcacca cttcacacag ggaaacgcaa aaggcatacc tgctggcagc 900  
gggggtcatt gtctgtatct atataatctg tgctgtcatc ctgatcctgg 950  
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gcctacttcc ggggcctacg gctggctatg agccacggcc catacatcaa 1050  
acttattact ggcttctct tccctcctt ggctttcatg ctggtggagg 1100  
ggaactttgt cttgttttgc acctacacct tgggcttccg caatgaattc 1150  
cagaatctac tcttgccat catgtctctg gccactttaa ccattcccat 1200  
ctggcagtgg ttcttgacct gggttgga gaagacagct gtatatgttg 1250

ggatctcatc agcagtgcc a tttctcatct tggtagccct catggagagt 1300  
 aacctcatca ttacatatgc ggtagctgtg gcagctggca tcagtgtggc 1350  
 agctgccttc ttactaccct ggtccatgct gcctgatgtc attgacgact 1400  
 tccatctgaa gcagccccac ttccatggaa ccgagcccat cttcttctcc 1450  
 ttctatgtct tcttcaccaa gtttgcctct ggagtgtcac tgggcatttc 1500  
 taccctcagt ctggactttg cagggtagca gacctgtggc tgctcgcagc 1550  
 cggaacgtgt caagtttaca ctgaacatgc tcgtgacct ggctcccata 1600  
 gttctcatcc tgctgggcct gctgctcttc aaaatgtacc ccattgatga 1650  
 ggagaggcgg cggcagaata agaaggccct gcaggcactg agggacgagg 1700  
 ccagcagctc tggctgctca gaaacagact ccacagagct ggctagcatc 1750  
 ctctagggcc cgccacgttg cccgaagcca ccattgcagaa ggccacagaa 1800  
 gggatcagga cctgtctgcc ggcttctgta gcagctggac tgcaggtgct 1850  
 aggaaggaa ctgaagactc aaggaggtgg cccaggacac ttgctgtgct 1900  
 cactgtgggg ccggctgctc tgtggcctcc tgcctccct ctgctgcct 1950  
 gtggggccaa gccctggggc tgccactgtg aatatgcaa ggactgatcg 2000  
 ggcctagccc ggaacactaa ttagaaaacc ttttttttac agagccta 2050  
 taataactta atgactgtgt acatagcaat gtgtgtgtat gtatatgtct 2100  
 gtgagctatt aatgttatta attttcataa aagctggaaa gc 2142

<210> 20  
 <211> 458  
 <212> PRT  
 <213> Homo sapiens

<400> 20  
 Met Trp Leu Arg Trp Ala Leu Ser Leu Pro Pro Ser Ser Cys Leu  
 1 5 10 15  
 Trp Ala Glu Pro Gly Met Pro Ser Gln Thr Pro Trp Trp Ala Ser  
 20 25 30  
 Ala Ser Ala Asn Pro Pro Gly Pro Ala Trp Val Ala Leu Cys Pro  
 35 40 45  
 Gly Ser Ser Ser Pro Arg Pro Trp Pro Ser Leu Pro Thr Ser Ser  
 50 55 60  
 Ser Gly Ser Cys Pro Thr Ser His Thr Ala Arg Pro Ile Gly Thr  
 65 70 75  
 Cys Phe Ser Ile Ala Ser Leu Lys Gln Trp Ser Arg Val Ser Met  
 80 85 90  
 Phe Pro Thr Arg Leu Ser Pro Cys Ser Ser Ala Thr Glu Gln Thr  
 95 100 105

Glu Arg Asp Ser Ala Thr Ala Tyr Arg Met Thr Val Glu Val Leu	110	115	120
Gly Thr Val Leu Gly Thr Ala Ile Gln Gly Gln Ile Val Gly Gln	125	130	135
Ala Asp Thr Pro Cys Phe Gln Asp Phe Asn Ser Ser Thr Val Ala	140	145	150
Ser Gln Ser Ala Asn His Thr His Gly Thr Thr Ser His Arg Glu	155	160	165
Thr Gln Lys Ala Tyr Leu Leu Ala Ala Gly Val Ile Val Cys Ile	170	175	180
Tyr Ile Ile Cys Ala Val Ile Leu Ile Leu Gly Val Arg Glu Gln	185	190	195
Arg Glu Pro Tyr Glu Ala Gln Gln Ser Glu Pro Ile Ala Tyr Phe	200	205	210
Arg Gly Leu Arg Leu Val Met Ser His Gly Pro Tyr Ile Lys Leu	215	220	225
Ile Thr Gly Phe Leu Phe Thr Ser Leu Ala Phe Met Leu Val Glu	230	235	240
Gly Asn Phe Val Leu Phe Cys Thr Tyr Thr Leu Gly Phe Arg Asn	245	250	255
Glu Phe Gln Asn Leu Leu Leu Ala Ile Met Leu Ser Ala Thr Leu	260	265	270
Thr Ile Pro Ile Trp Gln Trp Phe Leu Thr Arg Phe Gly Lys Lys	275	280	285
Thr Ala Val Tyr Val Gly Ile Ser Ser Ala Val Pro Phe Leu Ile	290	295	300
Leu Val Ala Leu Met Glu Ser Asn Leu Ile Ile Thr Tyr Ala Val	305	310	315
Ala Val Ala Ala Gly Ile Ser Val Ala Ala Ala Phe Leu Leu Pro	320	325	330
Trp Ser Met Leu Pro Asp Val Ile Asp Asp Phe His Leu Lys Gln	335	340	345
Pro His Phe His Gly Thr Glu Pro Ile Phe Phe Ser Phe Tyr Val	350	355	360
Phe Phe Thr Lys Phe Ala Ser Gly Val Ser Leu Gly Ile Ser Thr	365	370	375
Leu Ser Leu Asp Phe Ala Gly Tyr Gln Thr Arg Gly Cys Ser Gln	380	385	390
Pro Glu Arg Val Lys Phe Thr Leu Asn Met Leu Val Thr Met Ala	395	400	405
Pro Ile Val Leu Ile Leu Leu Gly Leu Leu Leu Phe Lys Met Tyr	410	415	420

Pro Ile Asp Glu Glu Arg Arg Arg Gln Asn Lys Lys Ala Leu Gln  
425 430 435

Ala Leu Arg Asp Glu Ala Ser Ser Ser Gly Cys Ser Glu Thr Asp  
440 445 450

Ser Thr Glu Leu Ala Ser Ile Leu  
455

<210> 21

<211> 571

<212> DNA

<213> Homo sapiens

<400> 21

gggaaacgca aaaggcatac ctgctggcag cgggggtcat tgtctgtatc 50  
tatataatct gtgctgtcat cctgatactg ggcgtgcggg agcagagaga 100  
accctatgaa gccagcagct ctgagccaat cgcctacttc cggggcctac 150  
ggctgggtcat gagccacggc ccatacatca aacttattac tggcttcctc 200  
ttcacctcct tggctttcat gctggtggag gggaactttg tcttgttttg 250  
cacctacacc ttgggcttcc gcaatgaatt ccagaatcta ctcttgcca 300  
tcatgctctc ggccacttta accattccca tctggcagtg gttcttgacc 350  
cggtttgga agaagacagc tgtatatgtt gggatctcat cagcagtgcc 400  
atttctcatc ttggtggccc tcatggagag taacctcatc attacatatg 450  
cggtagctgt ggcagctggc atcagtggtg cagctgcctt cttactaccc 500  
tgggccatgc tgcctgatgt cattgaagac ttccatctga agcagcccca 550  
cttccatgga accgagccca t 571

<210> 22

<211> 1173

<212> DNA

<213> Homo sapiens

<400> 22

ggggcttcgg cgccagcggc cagcgctagt cggctctggta aggatttaca 50  
aaaggtgcag gtatgagcag gtctgaagac taacattttg tgaagttgta 100  
aaacagaaaa cctgttagaa atgtgggtgtt ttcagcaagg cctcagtttc 150  
cttccttcag cccttgtaat ttggacatct gctgctttca tattttcata 200  
cattactgca gtaacactcc accatataga cccggcttta cottatatca 250  
gtgacactgg tacagtagct ccagaaaaat gcttatttgg ggcaatgcta 300  
aatattgcgg cagttttatg cattgctacc atttatgttc gttataagca 350  
agttcatgct ctgagtcctg aagagaacgt tatcatcaaa ttaaacaagg 400  
ctggccttgt acttggaata ctgagttgtt taggactttc tattgtggca 450



aacttccaga aaacaaccct ttttgctgca catgtaagtg gagctgtgct 500  
tacctttgggt atggggtcat tatatatgtt tgttcagacc atcctttcct 550  
accaaagtga gcccaaatc catggcaaac aagtcttctg gatcagactg 600  
ttgttggtta tctggtgtgg agtaagtga cttagcatgc tgacttgctc 650  
atcagttttg cacagtggca attttgggac tgatttagaa cagaaactcc 700  
attggaaccc cgaggacaaa ggttatgtgc ttcacatgat cactactgca 750  
gcagaatggt ctatgtcatt ttccttcttt gggtttttcc tgacttacat 800  
tcgtgatttt cagaaaatth ctttacgggt ggaagccaat ttacatggat 850  
taaccctcta tgacactgca ccttgcccta ttaacaatga acgaacacgg 900  
ctactttcca gagatatthg atgaaaggat aaaatatttc tgtaatgatt 950  
atgattotca gggattgggg aaagggtcac agaagttgct tattcttctc 1000  
tgaaatthtc aaccacttaa tcaaggctga cagtaacact gatgaatgct 1050  
gataatcagg aaacatgaaa gaagccattt gatagattat tctaaaggat 1100  
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gaaaataaag tcaaaagact atg 1173

<210> 23  
<211> 266  
<212> PRT  
<213> Homo sapiens

<400> 23  
Met Trp Trp Phe Gln Gln Gly Leu Ser Phe Leu Pro Ser Ala Leu  
1 5 10 15  
Val Ile Trp Thr Ser Ala Ala Phe Ile Phe Ser Tyr Ile Thr Ala  
20 25 30  
Val Thr Leu His His Ile Asp Pro Ala Leu Pro Tyr Ile Ser Asp  
35 40 45  
Thr Gly Thr Val Ala Pro Glu Lys Cys Leu Phe Gly Ala Met Leu  
50 55 60  
Asn Ile Ala Ala Val Leu Cys Ile Ala Thr Ile Tyr Val Arg Tyr  
65 70 75  
Lys Gln Val His Ala Leu Ser Pro Glu Glu Asn Val Ile Ile Lys  
80 85 90  
Leu Asn Lys Ala Gly Leu Val Leu Gly Ile Leu Ser Cys Leu Gly  
95 100 105  
Leu Ser Ile Val Ala Asn Phe Gln Lys Thr Thr Leu Phe Ala Ala  
110 115 120  
His Val Ser Gly Ala Val Leu Thr Phe Gly Met Gly Ser Leu Tyr  
125 130 135

Met	Phe	Val	Gln	Thr	Ile	Leu	Ser	Tyr	Gln	Met	Gln	Pro	Lys	Ile
				140					145					150
His	Gly	Lys	Gln	Val	Phe	Trp	Ile	Arg	Leu	Leu	Leu	Val	Ile	Trp
				155					160					165
Cys	Gly	Val	Ser	Ala	Leu	Ser	Met	Leu	Thr	Cys	Ser	Ser	Val	Leu
				170					175					180
His	Ser	Gly	Asn	Phe	Gly	Thr	Asp	Leu	Glu	Gln	Lys	Leu	His	Trp
				185					190					195
Asn	Pro	Glu	Asp	Lys	Gly	Tyr	Val	Leu	His	Met	Ile	Thr	Thr	Ala
				200					205					210
Ala	Glu	Trp	Ser	Met	Ser	Phe	Ser	Phe	Phe	Gly	Phe	Phe	Leu	Thr
				215					220					225
Tyr	Ile	Arg	Asp	Phe	Gln	Lys	Ile	Ser	Leu	Arg	Val	Glu	Ala	Asn
				230					235					240
Leu	His	Gly	Leu	Thr	Leu	Tyr	Asp	Thr	Ala	Pro	Cys	Pro	Ile	Asn
				245					250					255
Asn	Glu	Arg	Thr	Arg	Leu	Leu	Ser	Arg	Asp	Ile				
				260					265					

<210> 24  
 <211> 485  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 14, 484  
 <223> unknown base

<400> 24  
 cggacgcttg ggcngcgcca gcggccagcg ctagtcggtc tggtaagtgc 50  
 ctgatgccga gttccgtctc tcgggtcttt tcttggtccc aggcaaagcg 100  
 gagcggagat cctcaaacgg cctagtgttt cgcgcttccg gagaaaatca 150  
 gcgggtctaataaattcctct ggtttgttga agcagttacc aagaatcttc 200  
 aaccctttcc cacaaaagct aattgagtac acgttctgt tgagtacacg 250  
 ttcctgttga ttacaaaag gtgcaggtat gagcaggtct gaagactaac 300  
 attttgtgaa gttgtaaaac agaaaacctg ttagaaatgt ggtggtttca 350  
 gcaaggcctc agtttccttc cttcagccct tgtaatttgg acatctgctg 400  
 ctttcatatt ttcatacatt actgcagtaa cactccacca tatagaccgc 450  
 gctttacctt atatcagtga cactggtaca gtanc 485

<210> 25  
 <211> 40  
 <212> DNA  
 <213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 25  
acctgttaga aatgtggtg tttcagcaag gcctcagttt 40

<210> 26  
<211> 46  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 26  
ggagatagct gctatgggtt cttcaggcac aacttaacat gggaag 46

<210> 27  
<211> 1399  
<212> DNA  
<213> Homo sapiens

<400> 27  
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ctgccccgcg ggccggggtg cggagccgac atgcgcccgc ttctcggcct 100  
ccttctggtc ttgcgcggct gcaccttcgc cttgtacttg ctgtcgacgc 150  
gactgccccg cgggcggaga ctgggctcca ccgaggaggc tggaggcagg 200  
tcgctgtggt tcccctccga cctggcagag ctgcgggagc tctctgaggt 250  
ccttcgagag taccggaagg agcaccagge ctacgtgttc ctgctcttct 300  
gcggcgcccta cctctacaaa cagggttttg ccatccccgg ctccagcttc 350  
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gtgctgtgtg ttgacctcgg tgggtgccac atgctgctac ctgctctcca 450  
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tgcagtgtct tttcagaaag gacactctgc tcttgaaggt gtattacatc 1050  
 aggttttcaa accagccctg gtgtagcaga cactgcaaca gatgcctcct 1100  
 agaaaatgct gtttgtggcc gggcgcggtg gctcacgcct gtaatcccag 1150  
 cactttggga ggccgaggcc ggtgattcac aaggtcagga gttcaagacc 1200  
 agcctggcca agatggtgaa atcctgtctc taataaaaaat acaaaaatta 1250  
 gccaggcgtg gtggcaggca cctgtaatcc cagctactcg ggaggctgag 1300  
 gcaggagaat tgcttgaacc aaggtggcag aggttgacgt aagccaagat 1350  
 cacaccactg cactccagcc tgggtgatag agtgagacac tgtcttgac 1399

<210> 28  
 <211> 264  
 <212> PRT  
 <213> Homo sapiens

<400> 28  
 Met Arg Pro Leu Leu Gly Leu Leu Leu Val Phe Ala Gly Cys Thr  
 1 5 10 15  
 Phe Ala Leu Tyr Leu Leu Ser Thr Arg Leu Pro Arg Gly Arg Arg  
 20 25 30  
 Leu Gly Ser Thr Glu Glu Ala Gly Gly Arg Ser Leu Trp Phe Pro  
 35 40 45  
 Ser Asp Leu Ala Glu Leu Arg Glu Leu Ser Glu Val Leu Arg Glu  
 50 55 60  
 Tyr Arg Lys Glu His Gln Ala Tyr Val Phe Leu Leu Phe Cys Gly  
 65 70 75  
 Ala Tyr Leu Tyr Lys Gln Gly Phe Ala Ile Pro Gly Ser Ser Phe  
 80 85 90  
 Leu Asn Val Leu Ala Gly Ala Leu Phe Gly Pro Trp Leu Gly Leu  
 95 100 105  
 Leu Leu Cys Cys Val Leu Thr Ser Val Gly Ala Thr Cys Cys Tyr  
 110 115 120  
 Leu Leu Ser Ser Ile Phe Gly Lys Gln Leu Val Val Ser Tyr Phe  
 125 130 135  
 Pro Asp Lys Val Ala Leu Leu Gln Arg Lys Val Glu Glu Asn Arg  
 140 145 150  
 Asn Ser Leu Phe Phe Phe Leu Leu Phe Leu Arg Leu Phe Pro Met  
 155 160 165  
 Thr Pro Asn Trp Phe Leu Asn Leu Ser Ala Pro Ile Leu Asn Ile  
 170 175 180  
 Pro Ile Val Gln Phe Phe Phe Ser Val Leu Ile Gly Leu Ile Pro  
 185 190 195  
 Tyr Asn Phe Ile Cys Val Gln Thr Gly Ser Ile Leu Ser Thr Leu  
 200 205 210

Thr Ser Leu Asp Ala Leu Phe Ser Trp Asp Thr Val Phe Lys Leu  
 215 220 225

Leu Ala Ile Ala Met Val Ala Leu Ile Pro Gly Thr Leu Ile Lys  
 230 235 240

Lys Phe Ser Gln Lys His Leu Gln Leu Asn Glu Thr Ser Thr Ala  
 245 250 255

Asn His Ile His Ser Arg Lys Asp Thr  
 260

<210> 29  
 <211> 1292  
 <212> DNA  
 <213> Homo sapiens

<400> 29  
 ccgaggcggg aggagcccga gggggcgcgga gccccgcatg aatcattgta 50  
 gtcaatcatt ttccagttct cagccgctca gttgtgatca agggacacgt 100  
 ggtttccgaa ctgccagctc agaataggaa aataacttgg gattttatat 150  
 tggaagacat ggatcttgct gccaacgaga tcagcattta tgacaaactt 200  
 tcagagactg ttgatttggg gagacagacc ggccatcagt gtggcatgtc 250  
 agagaaggca attgaaaaat ttatcagaca gctgctggaa aagaatgaac 300  
 ctgagagacc cccccgcag tatcctctcc ttatagttgt gtataagggt 350  
 ctgcgaacct tgggattaat cttgctcact gcctactttg tgattcaacc 400  
 tttcagccca ttagcacctg agccagtgtt ttctggagct cacacctggc 450  
 gctcactcat ccatcacatt aggctgatgt ccttgcccat tgccaagaag 500  
 tacatgtcag aaaataaggg agttcctctg catgggggtg atgaagacag 550  
 accctttcca gactttgacc cctggtggac aaacgactgt gagcagaatg 600  
 agtcagagcc cattcctgcc aactgcactg gctgtgcca gaaacacctg 650  
 aaggatgatg tcttggaaga cgccccagg aaatttgaga ggctccatcc 700  
 actggtgatc aagacgggaa agcccctgtt ggaggaagag attcagcatt 750  
 ttttgtgcca gtaccctgag gcgacagaag gcttctctga agggtttttc 800  
 gccaaagtggg ggcgctgctt tctgagcgg tggttcccat ttccttatcc 850  
 atggaggaga cctctgaaca gatcaciaat gttacgtgag ctttttctctg 900  
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 tttcttcacc cagaacctgt tgtggggagt aagatgcata agatgcctga 1000  
 cctattttatc attggcagcg gtgaggccat gttgcagctc atccctccct 1050  
 tccagtgccg aagacattgt cagtctgtgg ccattgccaat agagccaggg 1100  
 gatatcggt atgtcgacac caccactgg aaggtctacg ttatagccag 1150

aggggtccag ccttttggtca tctgcatgg aaccgctttc tcagaactgt 1200  
 aggaaataga actgtgcaca ggaacagctt ccagagccga aaaccagggt 1250  
 gaaaggggaa aaataaaaaac aaaaacgatg aaactgcaaa aa 1292

<210> 30  
 <211> 347  
 <212> PRT  
 <213> Homo sapiens

<400> 30  
 Met Asp Leu Ala Ala Asn Glu Ile Ser Ile Tyr Asp Lys Leu Ser 15  
 1 5 10  
 Glu Thr Val Asp Leu Val Arg Gln Thr Gly His Gln Cys Gly Met 30  
 20 25  
 Ser Glu Lys Ala Ile Glu Lys Phe Ile Arg Gln Leu Leu Glu Lys 45  
 35 40  
 Asn Glu Pro Gln Arg Pro Pro Pro Gln Tyr Pro Leu Leu Ile Val 60  
 50 55  
 Val Tyr Lys Val Leu Ala Thr Leu Gly Leu Ile Leu Leu Thr Ala 75  
 65 70  
 Tyr Phe Val Ile Gln Pro Phe Ser Pro Leu Ala Pro Glu Pro Val 90  
 80 85  
 Leu Ser Gly Ala His Thr Trp Arg Ser Leu Ile His His Ile Arg 105  
 95 100  
 Leu Met Ser Leu Pro Ile Ala Lys Lys Tyr Met Ser Glu Asn Lys 120  
 110 115  
 Gly Val Pro Leu His Gly Gly Asp Glu Asp Arg Pro Phe Pro Asp 135  
 125 130  
 Phe Asp Pro Trp Trp Thr Asn Asp Cys Glu Gln Asn Glu Ser Glu 150  
 140 145  
 Pro Ile Pro Ala Asn Cys Thr Gly Cys Ala Gln Lys His Leu Lys 165  
 155 160  
 Val Met Leu Leu Glu Asp Ala Pro Arg Lys Phe Glu Arg Leu His 180  
 170 175  
 Pro Leu Val Ile Lys Thr Gly Lys Pro Leu Leu Glu Glu Glu Ile 195  
 185 190  
 Gln His Phe Leu Cys Gln Tyr Pro Glu Ala Thr Glu Gly Phe Ser 210  
 200 205  
 Glu Gly Phe Phe Ala Lys Trp Trp Arg Cys Phe Pro Glu Arg Trp 225  
 215 220  
 Phe Pro Phe Pro Tyr Pro Trp Arg Arg Pro Leu Asn Arg Ser Gln 240  
 230 235  
 Met Leu Arg Glu Leu Phe Pro Val Phe Thr His Leu Pro Phe Pro 255  
 245 250

Lys	Asp	Ala	Ser	Leu	Asn	Lys	Cys	Ser	Phe	Leu	His	Pro	Glu	Pro
				260					265					270
Val	Val	Gly	Ser	Lys	Met	His	Lys	Met	Pro	Asp	Leu	Phe	Ile	Ile
				275					280					285
Gly	Ser	Gly	Glu	Ala	Met	Leu	Gln	Leu	Ile	Pro	Pro	Phe	Gln	Cys
				290					295					300
Arg	Arg	His	Cys	Gln	Ser	Val	Ala	Met	Pro	Ile	Glu	Pro	Gly	Asp
				305					310					315
Ile	Gly	Tyr	Val	Asp	Thr	Thr	His	Trp	Lys	Val	Tyr	Val	Ile	Ala
				320					325					330
Arg	Gly	Val	Gln	Pro	Leu	Val	Ile	Cys	Asp	Gly	Thr	Ala	Phe	Ser
				335					340					345

Glu Leu

<210> 31  
 <211> 478  
 <212> DNA  
 <213> Homo sapiens

<400> 31  
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 gcccgagggg cgcgagcccc gcatgaatca ttgtagtcaa tcattttcca 100  
 gttctcagcc gttcagttgt gatcaaggga cacgtggttt ccgaactgcc 150  
 agctcagaat aggaaaataa cttgggattt tatattggaa gacatggatc 200  
 ttgctgcaa cgagatcagc atttatgaca aactttcaga gactgttgat 250  
 ttggtgagac agaccggcca tcaagtgtggc atgtcagaga aggcaattga 300  
 aaaatttatc agacagctgc tggaaaagaa tgaacctcag agaccccccc 350  
 cgcagtatcc tctccttata gttgtgtata aggttctcgc aaccttgga 400  
 ttaatcttgc tcaactgccta ctttgtgatt caacctttca gcccattagc 450  
 acctgagcca gtgctttgtg gagctcac 478

<210> 32  
 <211> 3531  
 <212> DNA  
 <213> Homo sapiens

<400> 32  
 cccacgcgtc cgcccacgcg tccggctgaa cacctcttct ttggagtcag 50  
 ccactgatga ggcagggtcc ccaattgcag ctgcagcagc tgcagcagct 100  
 gcagagcgct gtccttggt ggtgccactg gtgcgcacgc tgctagaccg 150  
 tgcctatgag ccgctggggc tgcagtgggg actgccctcc ctgccacca 200  
 ccaatggcag cccaccttc tttgaagact tccaggcttt ttgtgccaca 250

cccgaatggc gccacttcat cgacaaacag gtacagccaa ccatgtccca 300  
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 ggaatgcctg ctatgacatg cttatgagca gtgggcagcg gcgccagtgg 400  
 gagcgcgccc agagtgcgtg ggccttccag gagctggtgc tggaacctgc 450  
 gcagagggcg gcgcgcctgg aggggctacg ctacacggca gtgctgaagc 500  
 agcaggcaac gcagcactcc atggccctgc tgactgggg ggcgctgtgg 550  
 cgccagctcg ccagcccatg tggggcctgg gcgctgaggg aactcccat 600  
 cccccgtgg aaactgtcca gcgccgagac atattcacgc atgctgtga 650  
 agctggtgcc caaccatcac ttcgaccctc acctggaagc cagcgtctc 700  
 cgagacaatc tgggtgaggt tcccctgaca cccaccgagg aggcctcact 750  
 gcctctggca gtgaccaaag aggccaaagt gagcaccca cccgagttgc 800  
 tgcaggagga ccagctcggc gaggacgagc tggctgagct ggagaccccg 850  
 atggaggcag cagaactgga tgagcagcgt gagaagctgg tgctgtcggc 900  
 cgagtgccag ctggtgacgg tagtgccgt ggtcccagg ctgctggagg 950  
 tcaccacaca gaatgtatac ttctacgatg gcagcactga gcgcgtggaa 1000  
 accgaggagg gcatcggtta tgatttcgg cgccactgg ccagctgcg 1050  
 tgaggtccac ctgcggcgtt tcaacctgc cgttcagca cttgagctct 1100  
 tctttatcga tcaggccaac tacttctca acttcccatg caaggtgggc 1150  
 acgacccag tctcatctcc tagccagact ccgagacccc agcctggccc 1200  
 catcccacc cataccagg tacggaacca ggtgtactcg tggctcctgc 1250  
 gcctacggcc cccctctcaa ggctaccta gcagccgctc ccccaggag 1300  
 atgctgcgtg cctcaggcct taccagaaa tgggtacagc gtgagatatc 1350  
 caacttcgag tacttgatgc aactcaacac cattgcgggg cggaacctaca 1400  
 atgacctgtc tcagtacct gtgttcccct ggttctgca ggactacgtg 1450  
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 gccatcgggt gtggtgaacc ccaagcatgc ccagctcgtg agggagaagt 1550  
 atgaaagctt tgaggacca gcaggacca ttgacaagtt cactatggc 1600  
 acccactact ccaatgcagc aggcgtgatg cactacctca tccgctgga 1650  
 gcccttcacc tccctgcacg tccagctgca aagtggccgc tttgactgct 1700  
 ccgaccggca gttccactcg gtggcggcag cctggcaggc acgcctggag 1750  
 agocctgcc atgtgaagga gctcatccg gaattcttct actttcctga 1800  
 ctctctggag aaccagaacg gttttgacct gggctgtctc cagctgacca 1850



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acacctacac	gagtggatcg	acctcatctt	tggtacaag	cagcgggggc	2000
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cacatccaac	tcggctctca	gttgagggaag	cagcccatcg	ccttgcaagc	2200
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gacccacca	tgggcagcca	caagacgcag	cgactgctga	gtggcccgtg	2400
ggtgccaggc	agtgggtgtga	gtggacaagc	actggcagtg	gccccggatg	2450
gaaagctgct	attcagcggg	ggccactggg	atggcagcct	gcgggtgact	2500
gcactacccc	gtggcaagct	gttgagccag	ctcagctgcc	accttgatgt	2550
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ccggggacac	cacgtgcatg	gtgtggcggc	tcctgcatca	gggtggtctg	2650
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gatctgagga	tggaaactgtg	atcatacaca	ctgtacgccg	cggacagttt	2800
gtagcggcac	tacggcctct	gggtgccaca	ttccctggac	ctattttcca	2850
cctggcattg	gggtccgaag	gccagattgt	ggtacagagc	tcagcgtggg	2900
aacgtcctgg	ggcccaggtc	acctactcct	tgcacctgta	ttcagtcaat	2950
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ccgggaggcc	ccgcccagaa	gtcggcgggg	acccccggg	gtgggcagcc	3400
cagggggtga	gcggggccca	ccctgccag	ctcagggatt	ggcgggcgat	3450

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ggggccgccc tgagggccag cactggcgtc t 3531

<210> 33

<211> 1003

<212> PRT

<213> Homo sapiens

<400> 33

Met	Ser	Gln	Phe	Glu	Met	Asp	Thr	Tyr	Ala	Lys	Ser	His	Asp	Leu
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Met	Ser	Gly	Phe	Trp	Asn	Ala	Cys	Tyr	Asp	Met	Leu	Met	Ser	Ser
				20					25					30

Gly	Gln	Arg	Arg	Gln	Trp	Glu	Arg	Ala	Gln	Ser	Arg	Arg	Ala	Phe
				35					40					45

Gln	Glu	Leu	Val	Leu	Glu	Pro	Ala	Gln	Arg	Arg	Ala	Arg	Leu	Glu
				50					55					60

Gly	Leu	Arg	Tyr	Thr	Ala	Val	Leu	Lys	Gln	Gln	Ala	Thr	Gln	His
				65					70					75

Ser	Met	Ala	Leu	Leu	His	Trp	Gly	Ala	Leu	Trp	Arg	Gln	Leu	Ala
				80					85					90

Ser	Pro	Cys	Gly	Ala	Trp	Ala	Leu	Arg	Asp	Thr	Pro	Ile	Pro	Arg
				95					100					105

Trp	Lys	Leu	Ser	Ser	Ala	Glu	Thr	Tyr	Ser	Arg	Met	Arg	Leu	Lys
				110					115					120

Leu	Val	Pro	Asn	His	His	Phe	Asp	Pro	His	Leu	Glu	Ala	Ser	Ala
				125					130					135

Leu	Arg	Asp	Asn	Leu	Gly	Glu	Val	Pro	Leu	Thr	Pro	Thr	Glu	Glu
				140					145					150

Ala	Ser	Leu	Pro	Leu	Ala	Val	Thr	Lys	Glu	Ala	Lys	Val	Ser	Thr
				155					160					165

Pro	Pro	Glu	Leu	Leu	Gln	Glu	Asp	Gln	Leu	Gly	Glu	Asp	Glu	Leu
				170					175					180

Ala	Glu	Leu	Glu	Thr	Pro	Met	Glu	Ala	Ala	Glu	Leu	Asp	Glu	Gln
				185					190					195

Arg	Glu	Lys	Leu	Val	Leu	Ser	Ala	Glu	Cys	Gln	Leu	Val	Thr	Val
				200					205					210

Val	Ala	Val	Val	Pro	Gly	Leu	Leu	Glu	Val	Thr	Thr	Gln	Asn	Val
				215					220					225

Tyr	Phe	Tyr	Asp	Gly	Ser	Thr	Glu	Arg	Val	Glu	Thr	Glu	Glu	Gly
				230					235					240

Ile	Gly	Tyr	Asp	Phe	Arg	Arg	Pro	Leu	Ala	Gln	Leu	Arg	Glu	Val
				245					250					255

His	Leu	Arg	Arg	Phe	Asn	Leu	Arg	Arg	Ser	Ala	Leu	Glu	Leu	Phe
				260					265					270

Phe Ile Asp Gln	Ala Asn Tyr Phe Leu	Asn Phe Pro Cys Lys	Val
275	280	285	
Gly Thr Thr Pro	Val Ser Ser Pro Ser	Gln Thr Pro Arg Pro	Gln
290	295	300	
Pro Gly Pro Ile	Pro Pro His Thr Gln	Val Arg Asn Gln Val	Tyr
305	310	315	
Ser Trp Leu Leu	Arg Leu Arg Pro Pro	Ser Gln Gly Tyr Leu	Ser
320	325	330	
Ser Arg Ser Pro	Gln Glu Met Leu Arg	Ala Ser Gly Leu Thr	Gln
335	340	345	
Lys Trp Val Gln	Arg Glu Ile Ser Asn	Phe Glu Tyr Leu Met	Gln
350	355	360	
Leu Asn Thr Ile	Ala Gly Arg Thr Tyr	Asn Asp Leu Ser Gln	Tyr
365	370	375	
Pro Val Phe Pro	Trp Val Leu Gln Asp	Tyr Val Ser Pro Thr	Leu
380	385	390	
Asp Leu Ser Asn	Pro Ala Val Phe Arg	Asp Leu Ser Lys Pro	Ile
395	400	405	
Gly Val Val Asn	Pro Lys His Ala Gln	Leu Val Arg Glu Lys	Tyr
410	415	420	
Glu Ser Phe Glu	Asp Pro Ala Gly Thr	Ile Asp Lys Phe His	Tyr
425	430	435	
Gly Thr His Tyr	Ser Asn Ala Ala Gly	Val Met His Tyr Leu	Ile
440	445	450	
Arg Val Glu Pro	Phe Thr Ser Leu His	Val Gln Leu Gln Ser	Gly
455	460	465	
Arg Phe Asp Cys	Ser Asp Arg Gln Phe	His Ser Val Ala Ala	Ala
470	475	480	
Trp Gln Ala Arg	Leu Glu Ser Pro Ala	Asp Val Lys Glu Leu	Ile
485	490	495	
Pro Glu Phe Phe	Tyr Phe Pro Asp Phe	Leu Glu Asn Gln Asn	Gly
500	505	510	
Phe Asp Leu Gly	Cys Leu Gln Leu Thr	Asn Glu Lys Val Gly	Asp
515	520	525	
Val Val Leu Pro	Pro Trp Ala Ser Ser	Pro Glu Asp Phe Ile	Gln
530	535	540	
Gln His Arg Gln	Ala Leu Glu Ser Glu	Tyr Val Ser Ala His	Leu
545	550	555	
His Glu Trp Ile	Asp Leu Ile Phe Gly	Tyr Lys Gln Arg Gly	Pro
560	565	570	
Ala Ala Glu Glu	Ala Leu Asn Val Phe	Tyr Tyr Cys Thr Tyr	Glu
575	580	585	

Gly	Ala	Val	Asp	Leu	Asp	His	Val	Thr	Asp	Glu	Arg	Glu	Arg	Lys
				590					595					600
Ala	Leu	Glu	Gly	Ile	Ile	Ser	Asn	Phe	Gly	Gln	Thr	Pro	Cys	Gln
				605					610					615
Leu	Leu	Lys	Glu	Pro	His	Pro	Thr	Arg	Leu	Ser	Ala	Glu	Glu	Ala
				620					625					630
Ala	His	Arg	Leu	Ala	Arg	Leu	Asp	Thr	Asn	Ser	Pro	Ser	Ile	Phe
				635					640					645
Gln	His	Leu	Asp	Glu	Leu	Lys	Ala	Phe	Phe	Ala	Glu	Val	Thr	Val
				650					655					660
Ser	Ala	Ser	Gly	Leu	Leu	Gly	Thr	His	Ser	Trp	Leu	Pro	Tyr	Asp
				665					670					675
Arg	Asn	Ile	Ser	Asn	Tyr	Phe	Ser	Phe	Ser	Lys	Asp	Pro	Thr	Met
				680					685					690
Gly	Ser	His	Lys	Thr	Gln	Arg	Leu	Leu	Ser	Gly	Pro	Trp	Val	Pro
				695					700					705
Gly	Ser	Gly	Val	Ser	Gly	Gln	Ala	Leu	Ala	Val	Ala	Pro	Asp	Gly
				710					715					720
Lys	Leu	Leu	Phe	Ser	Gly	Gly	His	Trp	Asp	Gly	Ser	Leu	Arg	Val
				725					730					735
Thr	Ala	Leu	Pro	Arg	Gly	Lys	Leu	Leu	Ser	Gln	Leu	Ser	Cys	His
				740					745					750
Leu	Asp	Val	Val	Thr	Cys	Leu	Ala	Leu	Asp	Thr	Cys	Gly	Ile	Tyr
				755					760					765
Leu	Ile	Ser	Gly	Ser	Arg	Asp	Thr	Thr	Cys	Met	Val	Trp	Arg	Leu
				770					775					780
Leu	His	Gln	Gly	Gly	Leu	Ser	Val	Gly	Leu	Ala	Pro	Lys	Pro	Val
				785					790					795
Gln	Val	Leu	Tyr	Gly	His	Gly	Ala	Ala	Val	Ser	Cys	Val	Ala	Ile
				800					805					810
Ser	Thr	Glu	Leu	Asp	Met	Ala	Val	Ser	Gly	Ser	Glu	Asp	Gly	Thr
				815					820					825
Val	Ile	Ile	His	Thr	Val	Arg	Arg	Gly	Gln	Phe	Val	Ala	Ala	Leu
				830					835					840
Arg	Pro	Leu	Gly	Ala	Thr	Phe	Pro	Gly	Pro	Ile	Phe	His	Leu	Ala
				845					850					855
Leu	Gly	Ser	Glu	Gly	Gln	Ile	Val	Val	Gln	Ser	Ser	Ala	Trp	Glu
				860					865					870
Arg	Pro	Gly	Ala	Gln	Val	Thr	Tyr	Ser	Leu	His	Leu	Tyr	Ser	Val
				875					880					885
Asn	Gly	Lys	Leu	Arg	Ala	Ser	Leu	Pro	Leu	Ala	Glu	Gln	Pro	Thr
				890					895					900

Ala	Leu	Thr	Val	Thr	Glu	Asp	Phe	Val	Leu	Leu	Gly	Thr	Ala	Gln
				905					910					915
Cys	Ala	Leu	His	Ile	Leu	Gln	Leu	Asn	Thr	Leu	Leu	Pro	Ala	Ala
				920					925					930
Pro	Pro	Leu	Pro	Met	Lys	Val	Ala	Ile	Arg	Ser	Val	Ala	Val	Thr
				935					940					945
Lys	Glu	Arg	Ser	His	Val	Leu	Val	Gly	Leu	Glu	Asp	Gly	Lys	Leu
				950					955					960
Ile	Val	Val	Val	Ala	Gly	Gln	Pro	Ser	Glu	Val	Arg	Ser	Ser	Gln
				965					970					975
Phe	Ala	Arg	Lys	Leu	Trp	Arg	Ser	Ser	Arg	Arg	Ile	Ser	Gln	Val
				980					985					990
Ser	Ser	Gly	Glu	Thr	Glu	Tyr	Asn	Pro	Thr	Glu	Ala	Arg		
				995					1000					

<210> 34  
 <211> 43  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 34  
 tgactgcact accccgtggc aagctgttga gccagctcag ctg 43

<210> 35  
 <211> 1395  
 <212> DNA  
 <213> Homo sapiens

<400> 35  
 cggacgcgtg ggcggacgcg tgggggctgt gagaaagtgc caataaatac 50  
 atcatgcaac cccacggccc accttgtgaa ctctctgtgc ccagggtga 100  
 tgtgctgtt ccagggtac tcatccaaag gcctaatacca acgttctgtc 150  
 ttcaatctgc aaatctatgg ggtcctgggg ctcttctgga cccttaactg 200  
 ggtactggcc ctgggccaat gcgtcctcgc tggagccttt gcctccttct 250  
 actgggcctt ccacaagccc caggacatcc ctaccttccc cttaatctct 300  
 gccttcatcc gcacactccg ttaccacact gggtcattgg catttgagc 350  
 cctcatcctg acccttgtgc agatagccc ggtcatcttg gagtatattg 400  
 accacaagct cagaggagtg cagaaccctg tagcccgtg catcatgtgc 450  
 tgtttcaagt gctgcctctg gtgtctggaa aaatttatca agttcctaaa 500  
 ccgcaatgca tacatcatga tcgccatcta cggaagaat ttctgtgtct 550  
 cagccaaaaa tgcgttcacg ctactcatgc gaaacattgt cagggtggtc 600  
 gtccctggaca aagtcacaga cctgctgctg ttctttggga agctgctggt 650

ggtcggaggc gtgggggtcc tgtccttctt ttttttctcc ggtcgcaccc 700  
 cggggctggg taaagacttt aagagccccc acctcaacta ttactggctg 750  
 cccatcatga cctccatcct gggggcctat gtcacgcga gcggcttctt 800  
 cagcgttttc ggcatgtgtg tggacacgct cttcctctgc ttcttggaag 850  
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 agccttctaa agattctggg caagaagaac gaggcgcccc cggacaacaa 950  
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 cccaccgtcc agccatccaa ctcacttcg ccttacagggt ctccattttg 1050  
 tggtaaaaaa aggttttagg ccaggcgccg tggtcacgc ctgtaatcca 1100  
 acactttgag aggctgaggc gggcggtatca cctgagtcag gagttcgaga 1150  
 ccagcctggc caacatggtg aaacctccgt ctctattaaa aatacaaaaa 1200  
 ttagccgaga gtggtggcat gcacctgtca tcccagctac tcgggagggt 1250  
 gaggcaggag aatcgcttga acccgggagg cagaggttgc agtgagccga 1300  
 gatcgcgcca ctgcactcca acctgggtga cagactctgt ctccaaaaca 1350  
 aaacaaacaa acaaaaagat tttattaaag atattttgtt aactc 1395

<210> 36  
 <211> 321  
 <212> PRT  
 <213> Homo sapiens

<400> 36  
 Arg Thr Arg Gly Arg Thr Arg Gly Gly Cys Glu Lys Val Pro Ile  
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 Asn Thr Ser Cys Asn Pro Thr Ala His Leu Val Asn Ser Ser Cys  
 20 25 30  
 Pro Gly Leu Met Cys Val Phe Gln Gly Tyr Ser Ser Lys Gly Leu  
 35 40 45  
 Ile Gln Arg Ser Val Phe Asn Leu Gln Ile Tyr Gly Val Leu Gly  
 50 55 60  
 Leu Phe Trp Thr Leu Asn Trp Val Leu Ala Leu Gly Gln Cys Val  
 65 70 75  
 Leu Ala Gly Ala Phe Ala Ser Phe Tyr Trp Ala Phe His Lys Pro  
 80 85 90  
 Gln Asp Ile Pro Thr Phe Pro Leu Ile Ser Ala Phe Ile Arg Thr  
 95 100 105  
 Leu Arg Tyr His Thr Gly Ser Leu Ala Phe Gly Ala Leu Ile Leu  
 110 115 120  
 Thr Leu Val Gln Ile Ala Arg Val Ile Leu Glu Tyr Ile Asp His  
 125 130 135

Lys	Leu	Arg	Gly	Val	Gln	Asn	Pro	Val	Ala	Arg	Cys	Ile	Met	Cys	
				140					145					150	
Cys	Phe	Lys	Cys	Cys	Leu	Trp	Cys	Leu	Glu	Lys	Phe	Ile	Lys	Phe	
				155					160					165	
Leu	Asn	Arg	Asn	Ala	Tyr	Ile	Met	Ile	Ala	Ile	Tyr	Gly	Lys	Asn	
				170					175					180	
Phe	Cys	Val	Ser	Ala	Lys	Asn	Ala	Phe	Met	Leu	Leu	Met	Arg	Asn	
				185					190					195	
Ile	Val	Arg	Val	Val	Val	Leu	Asp	Lys	Val	Thr	Asp	Leu	Leu	Leu	
				200					205					210	
Phe	Phe	Gly	Lys	Leu	Leu	Val	Val	Gly	Gly	Val	Gly	Val	Leu	Ser	
				215					220					225	
Phe	Phe	Phe	Phe	Ser	Gly	Arg	Ile	Pro	Gly	Leu	Gly	Lys	Asp	Phe	
				230					235					240	
Lys	Ser	Pro	His	Leu	Asn	Tyr	Tyr	Trp	Leu	Pro	Ile	Met	Thr	Ser	
				245					250					255	
Ile	Leu	Gly	Ala	Tyr	Val	Ile	Ala	Ser	Gly	Phe	Phe	Ser	Val	Phe	
				260					265					270	
Gly	Met	Cys	Val	Asp	Thr	Leu	Phe	Leu	Cys	Phe	Leu	Glu	Asp	Leu	
				275					280					285	
Glu	Arg	Asn	Asn	Gly	Ser	Leu	Asp	Arg	Pro	Tyr	Tyr	Met	Ser	Lys	
				290					295					300	
Ser	Leu	Leu	Lys	Ile	Leu	Gly	Lys	Lys	Asn	Glu	Ala	Pro	Pro	Asp	
				305					310					315	
Asn	Lys	Lys	Arg	Lys	Lys										
				320											

<210> 37  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 37  
 tcgtgccag gggctgatgt gc 22

<210> 38  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 38  
 gtctttaccc agccccggga tgcg 24

<210> 39  
 <211> 50

<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 39  
ggcctaatcc aacgttctgt cttcaatctg caaatctatg gggtcctggg 50

<210> 40  
<211> 1365  
<212> DNA  
<213> Homo sapiens

<400> 40  
gagtcttgac cgccgccggg ctcttggtac ctcagcgca ggcgcaggcg 50  
tccggccgcc gtggctatgt tcgtgtccga tttccgcaaa gagttctacg 100  
aggtgggtcca gagccagagg gtccttctct tcgtggcctc ggacgtggat 150  
gctctgtgtg cgtgcaagat ccttcaggcc ttgttccagt gtgaccacgt 200  
gcaatatacg ctggttccag tttctgggtg gcaagaactt gaaactgcat 250  
ttcttgagca taaagaacag tttcattatt ttattctcat aaactgtgga 300  
gctaattgtag acctattgga tattcttcaa cctgatgaag aactatatt 350  
ctttgtgtgt gactcccata ggccagtcaa tgcgtcaat gtatacaacg 400  
ataccagat caaattactc attaaacaag atgatgacct tgaagttccc 450  
gcctatgaag acatcttcag ggatgaagag gaggatgaag agcattcagg 500  
aaatgacagt gatgggtcag agccttctga gaagcgaca cggttagaag 550  
aggagatagt ggagcaaacc atgcggagga ggcagcggcg agagtgggag 600  
gcccggagaa gagacatcct ctttgactac gagcagtatg aatatcatgg 650  
gacatcgtca gccatggtga tgtttgagct ggcttgatg ctgtccaagg 700  
acctgaatga catgctgtgg tgggccatcg ttggactaac agaccagtgg 750  
gtgcaagaca agatcactca aatgaaatac gtgactgatg ttggtgtcct 800  
gcagcgccac gtttcccgcc acaaccaccg gaacgaggat gaggagaaca 850  
cactctccgt ggactgcaca cggatctcct ttgagtatga cctccgcctg 900  
gtgctctacc agcactggtc cctccatgac agcctgtgca acaccagcta 950  
taccgcagcc aggttcaagc tgtggtctgt gcatggacag aagcggctcc 1000  
aggagtccct tgcagacatg ggtcttcccc tgaagcaggt gaagcagaag 1050  
ttccaggcca tggacatctc cttgaaggag aatttgcgga aatgattga 1100  
agagtctgca aataaatttg ggatgaagga catgcgcgtg cagactttca 1150  
gcattcattt tgggttcaag cacaagtttc tggccagcga cgtggtcttt 1200



gccaccatgt ctttgatgga gagccccgag aaggatggct cagggacaga 1250  
 tcacttcata caggctctgg acagcctctc caggagtaac ctggacaagc 1300  
 tgtaccatgg cctggaactc gccagaagc agctgagcag caccagcag 1350  
 accattgcca gctgc 1365

<210> 41  
 <211> 566  
 <212> PRT  
 <213> Homo sapiens

<400> 41  
 Met Phe Val Ser Asp Phe Arg Lys Glu Phe Tyr Glu Val Val Gln  
 1 5 10 15  
 Ser Gln Arg Val Leu Leu Phe Val Ala Ser Asp Val Asp Ala Leu  
 20 25 30  
 Cys Ala Cys Lys Ile Leu Gln Ala Leu Phe Gln Cys Asp His Val  
 35 40 45  
 Gln Tyr Thr Leu Val Pro Val Ser Gly Trp Gln Glu Leu Glu Thr  
 50 55 60  
 Ala Phe Leu Glu His Lys Glu Gln Phe His Tyr Phe Ile Leu Ile  
 65 70 75  
 Asn Cys Gly Ala Asn Val Asp Leu Leu Asp Ile Leu Gln Pro Asp  
 80 85 90  
 Glu Asp Thr Ile Phe Phe Val Cys Asp Ser His Arg Pro Val Asn  
 95 100 105  
 Val Val Asn Val Tyr Asn Asp Thr Gln Ile Lys Leu Leu Ile Lys  
 110 115 120  
 Gln Asp Asp Asp Leu Glu Val Pro Ala Tyr Glu Asp Ile Phe Arg  
 125 130 135  
 Asp Glu Glu Glu Asp Glu Glu His Ser Gly Asn Asp Ser Asp Gly  
 140 145 150  
 Ser Glu Pro Ser Glu Lys Arg Thr Arg Leu Glu Glu Glu Ile Val  
 155 160 165  
 Glu Gln Thr Met Arg Arg Arg Gln Arg Arg Glu Trp Glu Ala Arg  
 170 175 180  
 Arg Arg Asp Ile Leu Phe Asp Tyr Glu Gln Tyr Glu Tyr His Gly  
 185 190 195  
 Thr Ser Ser Ala Met Val Met Phe Glu Leu Ala Trp Met Leu Ser  
 200 205 210  
 Lys Asp Leu Asn Asp Met Leu Trp Trp Ala Ile Val Gly Leu Thr  
 215 220 225  
 Asp Gln Trp Val Gln Asp Lys Ile Thr Gln Met Lys Tyr Val Thr  
 230 235 240  
 Asp Val Gly Val Leu Gln Arg His Val Ser Arg His Asn His Arg

245									250					255				
Asn	Glu	Asp	Glu	Glu 260	Asn	Thr	Leu	Ser	Val 265	Asp	Cys	Thr	Arg	Ile 270				
Ser	Phe	Glu	Tyr	Asp 275	Leu	Arg	Leu	Val	Leu 280	Tyr	Gln	His	Trp	Ser 285				
Leu	His	Asp	Ser	Leu 290	Cys	Asn	Thr	Ser	Tyr 295	Thr	Ala	Ala	Arg	Phe 300				
Lys	Leu	Trp	Ser	Val 305	His	Gly	Gln	Lys	Arg 310	Leu	Gln	Glu	Phe	Leu 315				
Ala	Asp	Met	Gly	Leu 320	Pro	Leu	Lys	Gln	Val 325	Lys	Gln	Lys	Phe	Gln 330				
Ala	Met	Asp	Ile	Ser 335	Leu	Lys	Glu	Asn	Leu 340	Arg	Glu	Met	Ile	Glu 345				
Glu	Ser	Ala	Asn	Lys 350	Phe	Gly	Met	Lys	Asp 355	Met	Arg	Val	Gln	Thr 360				
Phe	Ser	Ile	His	Phe 365	Gly	Phe	Lys	His	Lys 370	Phe	Leu	Ala	Ser	Asp 375				
Val	Val	Phe	Ala	Thr 380	Met	Ser	Leu	Met	Glu 385	Ser	Pro	Glu	Lys	Asp 390				
Gly	Ser	Gly	Thr	Asp 395	His	Phe	Ile	Gln	Ala 400	Leu	Asp	Ser	Leu	Ser 405				
Arg	Ser	Asn	Leu	Asp 410	Lys	Leu	Tyr	His	Gly 415	Leu	Glu	Leu	Ala	Lys 420				
Lys	Gln	Leu	Arg	Ala 425	Thr	Gln	Gln	Thr	Ile 430	Ala	Ser	Cys	Leu	Cys 435				
Thr	Asn	Leu	Val	Ile 440	Ser	Gln	Gly	Pro	Phe 445	Leu	Tyr	Cys	Ser	Leu 450				
Met	Glu	Gly	Thr	Pro 455	Asp	Val	Met	Leu	Phe 460	Ser	Arg	Pro	Ala	Ser 465				
Leu	Ser	Leu	Leu	Ser 470	Lys	His	Leu	Leu	Lys 475	Ser	Phe	Val	Cys	Ser 480				
Thr	Lys	Asn	Arg	Arg 485	Cys	Lys	Leu	Leu	Pro 490	Leu	Val	Met	Ala	Ala 495				
Pro	Leu	Ser	Met	Glu 500	His	Gly	Thr	Val	Thr 505	Val	Val	Gly	Ile	Pro 510				
Pro	Glu	Thr	Asp	Ser 515	Ser	Asp	Arg	Lys	Asn 520	Phe	Phe	Gly	Arg	Ala 525				
Phe	Glu	Lys	Ala	Ala 530	Glu	Ser	Thr	Ser	Ser 535	Arg	Met	Leu	His	Asn 540				
His	Phe	Asp	Leu	Ser 545	Val	Ile	Glu	Leu	Lys 550	Ala	Glu	Asp	Arg	Ser 555				
Lys	Phe	Leu	Asp	Ala	Leu	Ile	Ser	Leu	Leu	Ser								

<210> 42  
 <211> 380  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 44, 118, 172, 183  
 <223> unknown base

<400> 42  
 gtacctcagc gcgagcgcca ggcgtccggc cgccgtggct atgntcgtgt 50  
 ccgatttccg caaagagttc tacgaggtgg tccagagcca gagggtcctt 100  
 ctcttcgtgg cctcggangt ggatgctctg tgtgcgtgca agatccttca 150  
 ggccttgttc cagtgtgacc angtgcaata tangctgggt ccagtttctg 200  
 ggtggcaaga acttgaaact gcatttcttg agcataaaga acagtttcat 250  
 tattttattc tcataaactg tggagctaata gtagacctat tggatattct 300  
 tcaacctgat gaagacacta tattctttgt gtgtgacacc cataggccag 350  
 tcaatgttgt caatgtatac aacgataccc 380

<210> 43  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 43  
 ttccgcaaag agttctacga ggtgg 25

<210> 44  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 44  
 attgacaaca ttgactggcc tatggg 26

<210> 45  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 45  
 gtggatgctc tgtgtgcgtg caagatcctt caggccttgt tccagtgtga 50

<210> 46

<211> 3089  
<212> DNA  
<213> Homo sapiens

<400> 46  
caggaaccct ctcttttgggt ctggattggg acccctttcc agtaccattt 50  
tttctagtga accacgaagg gacgatacca gaaaacaccc tcaacccaaa 100  
ggaaatagac tacagcccca attggctgac tttggctata gaaaaaagaa 150  
aggaacgaaa agagacagtt ttttttggaa agctaagtct tccctttatc 200  
gagtcaagaa accccccctt cttgagctat ttacagcttt taacaattga 250  
gtaaagtacg ctccggtcac catggtgaca gccgccctgg gtcccgctctg 300  
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 cccctcttct cttgctcagg cctgcaccac tgcagccacc gttcatttat 1950  
 tcattcatta aacactgagc actcactctg tgctgggtcc cgggaagggt 2000  
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 ccaactgctcc ccaaggctgg tgggacggg tcccgggtggc aggggcaggt 2200  
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 accccagggg gccttgcca ggtcaagggt tctgtgagga gaggacccag 2300  
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 caaccatago tctccccaca gctgatacgg catcctgcga gaagacctgc 2400  
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 cttgctcagt cccttcacc aaagtcatct gaacttccgt tccccaggg 2500  
 cctccagctg ccctcagaca ctgatgtctg tccccaggtg ctctctgcc 2550  
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 tctctggtgc tcacagccga gggagccgtg gctccatggc cagatgacgg 2950  
 aaacagggtc tgaccaagtg ccaggaagac ctgtgctata aaccacctg 3000  
 cctgatcctg cccctgcctg acccggccac gccctgccgt ccagcatgat 3050

taaagaatgc tgtctcctct tggaaaaaaa aaaaaaaa 3089

<210> 47

<211> 259

<212> PRT

<213> Homo sapiens

<220>

<221> Signal Peptide

<222> 1-20

<223> Signal Peptide

<220>

<221> N-glycosylation Site

<222> 72-75

<223> N-glycosylation Site

<220>

<221> Clq Domain Proteins

<222> 144-178, 78-111, 84-117

<223> Clq Domain Proteins

<400> 47

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Phe Leu Leu Met Cys Glu Ile Arg Met Val Glu Leu Thr Phe Asp  
20 25 30

Arg Ala Val Ala Ser Gly Cys Gln Arg Cys Cys Asp Ser Glu Asp  
35 40 45

Pro Leu Asp Pro Ala His Val Ser Ser Ala Ser Ser Ser Gly Arg  
50 55 60

Pro His Ala Leu Pro Glu Ile Arg Pro Tyr Ile Asn Ile Thr Ile  
65 70 75

Leu Lys Gly Asp Lys Gly Asp Pro Gly Pro Met Gly Leu Pro Gly  
80 85 90

Tyr Met Gly Arg Glu Gly Pro Gln Gly Glu Pro Gly Pro Gln Gly  
95 100 105

Ser Lys Gly Asp Lys Gly Glu Met Gly Ser Pro Gly Ala Pro Cys  
110 115 120

Gln Lys Arg Phe Phe Ala Phe Ser Val Gly Arg Lys Thr Ala Leu  
125 130 135

His Ser Gly Glu Asp Phe Gln Thr Leu Leu Phe Glu Arg Val Phe  
140 145 150

Val Asn Leu Asp Gly Cys Phe Asp Met Ala Thr Gly Gln Phe Ala  
155 160 165

Ala Pro Leu Arg Gly Ile Tyr Phe Phe Ser Leu Asn Val His Ser  
170 175 180

Trp Asn Tyr Lys Glu Thr Tyr Val His Ile Met His Asn Gln Lys  
185 190 195

Glu Ala Val Ile Leu Tyr Ala Gln Pro Ser Glu Arg Ser Ile Met

	200		205		210
Gln Ser Gln Ser Val Met Leu Asp Leu Ala Tyr Gly Asp Arg Val					
	215		220		225
Trp Val Arg Leu Phe Lys Arg Gln Arg Glu Asn Ala Ile Tyr Ser					
	230		235		240
Asn Asp Phe Asp Thr Tyr Ile Thr Phe Ser Gly His Leu Ile Lys					
	245		250		255
Ala Glu Asp Asp					

<210> 48  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 48  
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<210> 49  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 49  
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<210> 50  
 <211> 50  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 50  
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<210> 51  
 <211> 2768  
 <212> DNA  
 <213> Homo sapiens

<400> 51  
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 ccgcctcccg ggacagaaga tgtgctccag ggtccctctg ctgctgccgc 150  
 tgctcctgct actggccctg gggcctgggg tgcagggctg cccatccggc 200  
 tgccagtgcg gccagccaca gacagtcttc tgactgccc gccaggggac 250

cacggtgccc cgagacgtgc caccgacac ggtggggctg tacgtctttg 300  
 agaacggcat caccatgctc gacgcaggca gctttgccgg cctgccgggc 350  
 ctgcagctcc tggacctgtc acagaaccag atcgccagcc tgcccagcgg 400  
 ggtcttccag ccactcgcca acctcagcaa cctggacctg acggccaaca 450  
 ggctgcatga aatcaccaat gagaccttcc gtggcctgcg gcgcctcgag 500  
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aaaagatgaa gtgtgaaa 2768

<210> 52  
<211> 673  
<212> PRT  
<213> Homo sapiens

<400> 52  
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Ser Gln Pro Gln Thr Val Phe Cys Thr Ala Arg Gln Gly Thr Thr  
35 40 45  
Val Pro Arg Asp Val Pro Pro Asp Thr Val Gly Leu Tyr Val Phe  
50 55 60  
Glu Asn Gly Ile Thr Met Leu Asp Ala Gly Ser Phe Ala Gly Leu  
65 70 75  
Pro Gly Leu Gln Leu Leu Asp Leu Ser Gln Asn Gln Ile Ala Ser  
80 85 90  
Leu Pro Ser Gly Val Phe Gln Pro Leu Ala Asn Leu Ser Asn Leu



	410		415		420
His Leu Gly Thr	Arg 425	His His Leu Ala	Cys 430	Leu Cys Pro Glu	Gly 435
Phe Thr Gly Leu	Tyr 440	Cys Glu Ser Gln	Met 445	Gly Gln Gly Thr	Arg 450
Pro Ser Pro Thr	Pro 455	Val Thr Pro Arg	Pro 460	Pro Arg Ser Leu	Thr 465
Leu Gly Ile Glu	Pro 470	Val Ser Pro Thr	Ser 475	Leu Arg Val Gly	Leu 480
Gln Arg Tyr Leu	Gln 485	Gly Ser Ser Val	Gln 490	Leu Arg Ser Leu	Arg 495
Leu Thr Tyr Arg	Asn 500	Leu Ser Gly Pro	Asp 505	Lys Arg Leu Val	Thr 510
Leu Arg Leu Pro	Ala 515	Ser Leu Ala Glu	Tyr 520	Thr Val Thr Gln	Leu 525
Arg Pro Asn Ala	Thr 530	Tyr Ser Val Cys	Val 535	Met Pro Leu Gly	Pro 540
Gly Arg Val Pro	Glu 545	Gly Glu Glu Ala	Cys 550	Gly Glu Ala His	Thr 555
Pro Pro Ala Val	His 560	Ser Asn His Ala	Pro 565	Val Thr Gln Ala	Arg 570
Glu Gly Asn Leu	Pro 575	Leu Leu Ile Ala	Pro 580	Ala Leu Ala Ala	Val 585
Leu Leu Ala Ala	Leu 590	Ala Ala Val Gly	Ala 595	Ala Tyr Cys Val	Arg 600
Arg Gly Arg Ala	Met 605	Ala Ala Ala Ala	Gln 610	Asp Lys Gly Gln	Val 615
Gly Pro Gly Ala	Gly 620	Pro Leu Glu Leu	Glu 625	Gly Val Lys Val	Pro 630
Leu Glu Pro Gly	Pro 635	Lys Ala Thr Glu	Gly 640	Gly Gly Glu Ala	Leu 645
Pro Ser Gly Ser	Glu 650	Cys Glu Val Pro	Leu 655	Met Gly Phe Pro	Gly 660
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<210> 53

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 53

tcttcagccg cttgcgcaac ctc 23

<210> 54  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 54  
ttgctcacat ccagctcctg cagg 24

<210> 55  
<211> 41  
<212> DNA  
<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

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<210> 56  
<211> 3462  
<212> DNA  
<213> Homo sapiens

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tggaaataca atgagactca tcagaaacat ttacatattt tgtagtattg 150  
ttatgacagc agagggtgat gctccagagc tgccagaaga aagggaactg 200  
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cataacagaa ttcaacagct ggatctcaaa acctttgaat tcaacaagga 400  
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<210> 57  
 <211> 811  
 <212> PRT  
 <213> Homo sapiens

<400> 57  
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 35 40 45  
 Leu Thr Pro Ala Thr Thr Thr Leu Asp Leu Ser Tyr Asn Leu Leu  
 50 55 60  
 Phe Gln Leu Gln Ser Ser Asp Phe His Ser Val Ser Lys Leu Arg  
 65 70 75  
 Val Leu Ile Leu Cys His Asn Arg Ile Gln Gln Leu Asp Leu Lys  
 80 85 90

Thr	Phe	Glu	Phe	Asn	Lys	Glu	Leu	Arg	Tyr	Leu	Asp	Leu	Ser	Asn	
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Asn	Arg	Leu	Lys	Ser	Val	Thr	Trp	Tyr	Leu	Leu	Ala	Gly	Leu	Arg	
				110					115					120	
Tyr	Leu	Asp	Leu	Ser	Phe	Asn	Asp	Phe	Asp	Thr	Met	Pro	Ile	Cys	
				125					130					135	
Glu	Glu	Ala	Gly	Asn	Met	Ser	His	Leu	Glu	Ile	Leu	Gly	Leu	Ser	
				140					145					150	
Gly	Ala	Lys	Ile	Gln	Lys	Ser	Asp	Phe	Gln	Lys	Ile	Ala	His	Leu	
				155					160					165	
His	Leu	Asn	Thr	Val	Phe	Leu	Gly	Phe	Arg	Thr	Leu	Pro	His	Tyr	
				170					175					180	
Glu	Glu	Gly	Ser	Leu	Pro	Ile	Leu	Asn	Thr	Thr	Lys	Leu	His	Ile	
				185					190					195	
Val	Leu	Pro	Met	Asp	Thr	Asn	Phe	Trp	Val	Leu	Leu	Arg	Asp	Gly	
				200					205					210	
Ile	Lys	Thr	Ser	Lys	Ile	Leu	Glu	Met	Thr	Asn	Ile	Asp	Gly	Lys	
				215					220					225	
Ser	Gln	Phe	Val	Ser	Tyr	Glu	Met	Gln	Arg	Asn	Leu	Ser	Leu	Glu	
				230					235					240	
Asn	Ala	Lys	Thr	Ser	Val	Leu	Leu	Leu	Asn	Lys	Val	Asp	Leu	Leu	
				245					250					255	
Trp	Asp	Asp	Leu	Phe	Leu	Ile	Leu	Gln	Phe	Val	Trp	His	Thr	Ser	
				260					265					270	
Val	Glu	His	Phe	Gln	Ile	Arg	Asn	Val	Thr	Phe	Gly	Gly	Lys	Ala	
				275					280					285	
Tyr	Leu	Asp	His	Asn	Ser	Phe	Asp	Tyr	Ser	Asn	Thr	Val	Met	Arg	
				290					295					300	
Thr	Ile	Lys	Leu	Glu	His	Val	His	Phe	Arg	Val	Phe	Tyr	Ile	Gln	
				305					310					315	
Gln	Asp	Lys	Ile	Tyr	Leu	Leu	Leu	Thr	Lys	Met	Asp	Ile	Glu	Asn	
				320					325					330	
Leu	Thr	Ile	Ser	Asn	Ala	Gln	Met	Pro	His	Met	Leu	Phe	Pro	Asn	
				335					340					345	
Tyr	Pro	Thr	Lys	Phe	Gln	Tyr	Leu	Asn	Phe	Ala	Asn	Asn	Ile	Leu	
				350					355					360	
Thr	Asp	Glu	Leu	Phe	Lys	Arg	Thr	Ile	Gln	Leu	Pro	His	Leu	Lys	
				365					370					375	
Thr	Leu	Ile	Leu	Asn	Gly	Asn	Lys	Leu	Glu	Thr	Leu	Ser	Leu	Val	
				380					385					390	
Ser	Cys	Phe	Ala	Asn	Asn	Thr	Pro	Leu	Glu	His	Leu	Asp	Leu	Ser	
				395					400					405	

Gln	Asn	Leu	Leu	Gln	His	Lys	Asn	Asp	Glu	Asn	Cys	Ser	Trp	Pro
				410					415					420
Glu	Thr	Val	Val	Asn	Met	Asn	Leu	Ser	Tyr	Asn	Lys	Leu	Ser	Asp
				425					430					435
Ser	Val	Phe	Arg	Cys	Leu	Pro	Lys	Ser	Ile	Gln	Ile	Leu	Asp	Leu
				440					445					450
Asn	Asn	Asn	Gln	Ile	Gln	Thr	Val	Pro	Lys	Glu	Thr	Ile	His	Leu
				455					460					465
Met	Ala	Leu	Arg	Glu	Leu	Asn	Ile	Ala	Phe	Asn	Phe	Leu	Thr	Asp
				470					475					480
Leu	Pro	Gly	Cys	Ser	His	Phe	Ser	Arg	Leu	Ser	Val	Leu	Asn	Ile
				485					490					495
Glu	Met	Asn	Phe	Ile	Leu	Ser	Pro	Ser	Leu	Asp	Phe	Val	Gln	Ser
				500					505					510
Cys	Gln	Glu	Val	Lys	Thr	Leu	Asn	Ala	Gly	Arg	Asn	Pro	Phe	Arg
				515					520					525
Cys	Thr	Cys	Glu	Leu	Lys	Asn	Phe	Ile	Gln	Leu	Glu	Thr	Tyr	Ser
				530					535					540
Glu	Val	Met	Met	Val	Gly	Trp	Ser	Asp	Ser	Tyr	Thr	Cys	Glu	Tyr
				545					550					555
Pro	Leu	Asn	Leu	Arg	Gly	Thr	Arg	Leu	Lys	Asp	Val	His	Leu	His
				560					565					570
Glu	Leu	Ser	Cys	Asn	Thr	Ala	Leu	Leu	Ile	Val	Thr	Ile	Val	Val
				575					580					585
Ile	Met	Leu	Val	Leu	Gly	Leu	Ala	Val	Ala	Phe	Cys	Cys	Leu	His
				590					595					600
Phe	Asp	Leu	Pro	Trp	Tyr	Leu	Arg	Met	Leu	Gly	Gln	Cys	Thr	Gln
				605					610					615
Thr	Trp	His	Arg	Val	Arg	Lys	Thr	Thr	Gln	Glu	Gln	Leu	Lys	Arg
				620					625					630
Asn	Val	Arg	Phe	His	Ala	Phe	Ile	Ser	Tyr	Ser	Glu	His	Asp	Ser
				635					640					645
Leu	Trp	Val	Lys	Asn	Glu	Leu	Ile	Pro	Asn	Leu	Glu	Lys	Glu	Asp
				650					655					660
Gly	Ser	Ile	Leu	Ile	Cys	Leu	Tyr	Glu	Ser	Tyr	Phe	Asp	Pro	Gly
				665					670					675
Lys	Ser	Ile	Ser	Glu	Asn	Ile	Val	Ser	Phe	Ile	Glu	Lys	Ser	Tyr
				680					685					690
Lys	Ser	Ile	Phe	Val	Leu	Ser	Pro	Asn	Phe	Val	Gln	Asn	Glu	Trp
				695					700					705
Cys	His	Tyr	Glu	Phe	Tyr	Phe	Ala	His	His	Asn	Leu	Phe	His	Glu
				710					715					720



Asn	Ser	Asp	His	Ile	Ile	Leu	Ile	Leu	Leu	Glu	Pro	Ile	Pro	Phe
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Tyr	Cys	Ile	Pro	Thr	Arg	Tyr	His	Lys	Leu	Lys	Ala	Leu	Leu	Glu
				740						745				750
Lys	Lys	Ala	Tyr	Leu	Glu	Trp	Pro	Lys	Asp	Arg	Arg	Lys	Cys	Gly
				755						760				765
Leu	Phe	Trp	Ala	Asn	Leu	Arg	Ala	Ala	Ile	Asn	Val	Asn	Val	Leu
				770						775				780
Ala	Thr	Arg	Glu	Met	Tyr	Glu	Leu	Gln	Thr	Phe	Thr	Glu	Leu	Asn
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Glu	Glu	Ser	Arg	Gly	Ser	Thr	Ile	Ser	Leu	Met	Arg	Thr	Asp	Cys
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Leu

<210> 58  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 58  
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<210> 59  
 <211> 27  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 59  
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<210> 60  
 <211> 40  
 <212> DNA  
 <213> Artificial Sequence

<220>  
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<400> 60  
 aaaaagcata cttggaatgg cccaaggata ggtgtaaagt 40

<210> 61  
 <211> 3772  
 <212> DNA  
 <213> Homo sapiens

<400> 61  
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<210> 62  
 <211> 756  
 <212> PRT  
 <213> Homo sapiens

<400> 62  
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 35 40 45  
 Tyr Tyr Ala Arg Pro Glu Pro Glu Leu Glu Thr Phe Ser Pro Pro  
 50 55 60  
 Leu Pro Ala Gly Pro Gly Glu Glu Trp Glu Arg Arg Pro Gln Glu  
 65 70 75  
 Pro Arg Pro Pro Lys Arg Ala Thr Lys Pro Lys Lys Ala Pro Lys  
 80 85 90  
 Arg Glu Lys Ser Ala Pro Glu Pro Pro Pro Pro Gly Lys His Ser  
 95 100 105  
 Asn Lys Lys Val Met Arg Thr Lys Ser Ser Glu Lys Ala Ala Asn  
 110 115 120  
 Asp Asp His Ser Val Arg Val Ala Arg Glu Asp Val Arg Glu Ser  
 125 130 135  
 Cys Pro Pro Leu Gly Leu Glu Thr Leu Lys Ile Thr Asp Phe Gln  
 140 145 150  
 Leu His Ala Ser Thr Val Lys Arg Tyr Gly Leu Gly Ala His Arg  
 155 160 165  
 Gly Arg Leu Asn Ile Gln Ala Gly Ile Asn Glu Asn Asp Phe Tyr  
 170 175 180  
 Asp Gly Ala Trp Cys Ala Gly Arg Asn Asp Leu Gln Gln Trp Ile



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Pro	Tyr	Asp	Leu	Val	Arg	Ser	Pro	Trp	Lys	Thr	Gln	Glu	His	Thr
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Pro	Thr	Pro	Asp	Asp	His	Val	Phe	Arg	Trp	Leu	Ala	Tyr	Ser	Tyr
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Ala	Ser	Thr	His	Arg	Leu	Met	Thr	Asp	Ala	Arg	Arg	Arg	Val	Cys
				560					565					570
His	Thr	Glu	Asp	Phe	Gln	Lys	Glu	Glu	Gly	Thr	Val	Asn	Gly	Ala
				575					580					585
Ser	Trp	His	Thr	Val	Ala	Gly	Ser	Leu	Asn	Asp	Phe	Ser	Tyr	Leu
				590					595					600
His	Thr	Asn	Cys	Phe	Glu	Leu	Ser	Ile	Tyr	Val	Gly	Cys	Asp	Lys
				605					610					615
Tyr	Pro	His	Glu	Ser	Gln	Leu	Pro	Glu	Glu	Trp	Glu	Asn	Asn	Arg
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Glu	Ser	Leu	Ile	Val	Phe	Met	Glu	Gln	Val	His	Arg	Gly	Ile	Lys
				635					640					645
Gly	Leu	Val	Arg	Asp	Ser	His	Gly	Lys	Gly	Ile	Pro	Asn	Ala	Ile
				650					655					660
Ile	Ser	Val	Glu	Gly	Ile	Asn	His	Asp	Ile	Arg	Thr	Ala	Asn	Asp
				665					670					675
Gly	Asp	Tyr	Trp	Arg	Leu	Leu	Asn	Pro	Gly	Glu	Tyr	Val	Val	Thr
				680					685					690
Ala	Lys	Ala	Glu	Gly	Phe	Thr	Ala	Ser	Thr	Lys	Asn	Cys	Met	Val
				695					700					705
Gly	Tyr	Asp	Met	Gly	Ala	Thr	Arg	Cys	Asp	Phe	Thr	Leu	Ser	Lys
				710					715					720
Thr	Asn	Met	Ala	Arg	Ile	Arg	Glu	Ile	Met	Glu	Lys	Phe	Gly	Lys
				725					730					735
Gln	Pro	Val	Ser	Leu	Pro	Ala	Arg	Arg	Leu	Lys	Leu	Arg	Gly	Arg
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Lys	Arg	Arg	Gln	Arg	Gly									
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<210> 63

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 63

gtttctcaatg agctacccgt cccc 24

<210> 64  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 64  
cgcatgtag tggaactcgg gctc 24

<210> 65  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 65  
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<210> 66  
<211> 2854  
<212> DNA  
<213> Homo sapiens

<400> 66  
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cagctccagc tccaggtcgg gctccagctc cagccgcagc ttaggcagcg 200  
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 ccacacttca ggtgctaaac acttggtata ccaagcagta taaaccatct 1300  
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aaaa 2854

<210> 67  
<211> 510  
<212> PRT  
<213> Homo sapiens

<400> 67  
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Ser Pro Gly Phe Ser Ser Phe Pro Gly Val Asp Ser Ser Ser Ser  
35 40 45  
Phe Ser Ser Ser Ser Arg Ser Gly Ser Ser Ser Ser Arg Ser Leu  
50 55 60  
Gly Ser Gly Gly Ser Val Ser Gln Leu Phe Ser Asn Phe Thr Gly  
65 70 75  
Ser Val Asp Asp Arg Gly Thr Cys Gln Cys Ser Val Ser Leu Pro  
80 85 90  
Asp Thr Thr Phe Pro Val Asp Arg Val Glu Arg Leu Glu Phe Thr  
95 100 105  
Ala His Val Leu Ser Gln Lys Phe Glu Lys Glu Leu Ser Lys Val  
110 115 120  
Arg Glu Tyr Val Gln Leu Ile Ser Val Tyr Glu Lys Lys Leu Leu  
125 130 135  
Asn Leu Thr Val Arg Ile Asp Ile Met Glu Lys Asp Thr Ile Ser  
140 145 150  
Tyr Thr Glu Leu Asp Phe Glu Leu Ile Lys Val Glu Val Lys Glu  
155 160 165  
Met Glu Lys Leu Val Ile Gln Leu Lys Glu Ser Phe Gly Gly Ser  
170 175 180  
Ser Glu Ile Val Asp Gln Leu Glu Val Glu Ile Arg Asn Met Thr  
185 190 195  
Leu Leu Val Glu Lys Leu Glu Thr Leu Asp Lys Asn Asn Val Leu  
200 205 210

Ala	Ile	Arg	Arg	Glu	Ile	Val	Ala	Leu	Lys	Thr	Lys	Leu	Lys	Glu	215	220	225
Cys	Glu	Ala	Ser	Lys	Asp	Gln	Asn	Thr	Pro	Val	Val	His	Pro	Pro	230	235	240
Pro	Thr	Pro	Gly	Ser	Cys	Gly	His	Gly	Gly	Val	Val	Asn	Ile	Ser	245	250	255
Lys	Pro	Ser	Val	Val	Gln	Leu	Asn	Trp	Arg	Gly	Phe	Ser	Tyr	Leu	260	265	270
Tyr	Gly	Ala	Trp	Gly	Arg	Asp	Tyr	Ser	Pro	Gln	His	Pro	Asn	Lys	275	280	285
Gly	Leu	Tyr	Trp	Val	Ala	Pro	Leu	Asn	Thr	Asp	Gly	Arg	Leu	Leu	290	295	300
Glu	Tyr	Tyr	Arg	Leu	Tyr	Asn	Thr	Leu	Asp	Asp	Leu	Leu	Leu	Tyr	305	310	315
Ile	Asn	Ala	Arg	Glu	Leu	Arg	Ile	Thr	Tyr	Gly	Gln	Gly	Ser	Gly	320	325	330
Thr	Ala	Val	Tyr	Asn	Asn	Asn	Met	Tyr	Val	Asn	Met	Tyr	Asn	Thr	335	340	345
Gly	Asn	Ile	Ala	Arg	Val	Asn	Leu	Thr	Thr	Asn	Thr	Ile	Ala	Val	350	355	360
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Ala	Asn	Val	Ala	Trp	Gln	Asp	Ile	Asp	Phe	Ala	Val	Asp	Glu	Asn	380	385	390
Gly	Leu	Trp	Val	Ile	Tyr	Ser	Thr	Glu	Ala	Ser	Thr	Gly	Asn	Met	395	400	405
Val	Ile	Ser	Lys	Leu	Asn	Asp	Thr	Thr	Leu	Gln	Val	Leu	Asn	Thr	410	415	420
Trp	Tyr	Thr	Lys	Gln	Tyr	Lys	Pro	Ser	Ala	Ser	Asn	Ala	Phe	Met	425	430	435
Val	Cys	Gly	Val	Leu	Tyr	Ala	Thr	Arg	Thr	Met	Asn	Thr	Arg	Thr	440	445	450
Glu	Glu	Ile	Phe	Tyr	Tyr	Tyr	Asp	Thr	Asn	Thr	Gly	Lys	Glu	Gly	455	460	465
Lys	Leu	Asp	Ile	Val	Met	His	Lys	Met	Gln	Glu	Lys	Val	Gln	Ser	470	475	480
Ile	Asn	Tyr	Asn	Pro	Phe	Asp	Gln	Lys	Leu	Tyr	Val	Tyr	Asn	Asp	485	490	495
Gly	Tyr	Leu	Leu	Asn	Tyr	Asp	Leu	Ser	Val	Leu	Gln	Lys	Pro	Gln	500	505	510

<210> 68  
 <211> 410  
 <212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 206, 217, 387

<223> unknown base

<400> 68

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<210> 69

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 69

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<210> 70

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 70

ctaccttggc cataggtgat ccgc 24

<210> 71

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 71

catcagcaaa ccgtctgtgg ttcagctcaa ctggagaggg tt 42

<210> 72

<211> 3127

<212> DNA

<213> Homo sapiens

<400> 72

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<210> 73  
 <211> 453  
 <212> PRT  
 <213> Homo sapiens

<400> 73

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Cys	Leu	Cys	Gly	Ser	Ala	Pro	Cys	Leu	Leu	Cys	Arg	Cys	Cys	Pro	20	25	30	
Ser	Gly	Asn	Asn	Ser	Thr	Val	Thr	Arg	Leu	Ile	Tyr	Ala	Leu	Phe	35	40	45	
Leu	Leu	Val	Gly	Val	Cys	Val	Ala	Cys	Val	Met	Leu	Ile	Pro	Gly	50	55	60	
Met	Glu	Glu	Gln	Leu	Asn	Lys	Ile	Pro	Gly	Phe	Cys	Glu	Asn	Glu	65	70	75	
Lys	Gly	Val	Val	Pro	Cys	Asn	Ile	Leu	Val	Gly	Tyr	Lys	Ala	Val	80	85	90	
Tyr	Arg	Leu	Cys	Phe	Gly	Leu	Ala	Met	Phe	Tyr	Leu	Leu	Leu	Ser	95	100	105	
Leu	Leu	Met	Ile	Lys	Val	Lys	Ser	Ser	Ser	Asp	Pro	Arg	Ala	Ala	110	115	120	
Val	His	Asn	Gly	Phe	Trp	Phe	Phe	Lys	Phe	Ala	Ala	Ala	Ile	Ala	125	130	135	
Ile	Ile	Ile	Gly	Ala	Phe	Phe	Ile	Pro	Glu	Gly	Thr	Phe	Thr	Thr	140	145	150	
Val	Trp	Phe	Tyr	Val	Gly	Met	Ala	Gly	Ala	Phe	Cys	Phe	Ile	Leu	155	160	165	
Ile	Gln	Leu	Val	Leu	Leu	Ile	Asp	Phe	Ala	His	Ser	Trp	Asn	Glu	170	175	180	
Ser	Trp	Val	Glu	Lys	Met	Glu	Glu	Gly	Asn	Ser	Arg	Cys	Trp	Tyr	185	190	195	
Ala	Ala	Leu	Leu	Ser	Ala	Thr	Ala	Leu	Asn	Tyr	Leu	Leu	Ser	Leu	200	205	210	
Val	Ala	Ile	Val	Leu	Phe	Phe	Val	Tyr	Tyr	Thr	His	Pro	Ala	Ser	215	220	225	
Cys	Ser	Glu	Asn	Lys	Ala	Phe	Ile	Ser	Val	Asn	Met	Leu	Leu	Cys	230	235	240	
Val	Gly	Ala	Ser	Val	Met	Ser	Ile	Leu	Pro	Lys	Ile	Gln	Glu	Ser	245	250	255	
Gln	Pro	Arg	Ser	Gly	Leu	Leu	Gln	Ser	Ser	Val	Ile	Thr	Val	Tyr	260	265	270	
Thr	Met	Tyr	Leu	Thr	Trp	Ser	Ala	Met	Thr	Asn	Glu	Pro	Glu	Thr	275	280	285	

Asn	Cys	Asn	Pro	Ser	Leu	Leu	Ser	Ile	Ile	Gly	Tyr	Asn	Thr	Thr	290	295	300
Ser	Thr	Val	Pro	Lys	Glu	Gly	Gln	Ser	Val	Gln	Trp	Trp	His	Ala	305	310	315
Gln	Gly	Ile	Ile	Gly	Leu	Ile	Leu	Phe	Leu	Leu	Cys	Val	Phe	Tyr	320	325	330
Ser	Ser	Ile	Arg	Thr	Ser	Asn	Asn	Ser	Gln	Val	Asn	Lys	Leu	Thr	335	340	345
Leu	Thr	Ser	Asp	Glu	Ser	Thr	Leu	Ile	Glu	Asp	Gly	Gly	Ala	Arg	350	355	360
Ser	Asp	Gly	Ser	Leu	Glu	Asp	Gly	Asp	Asp	Val	His	Arg	Ala	Val	365	370	375
Asp	Asn	Glu	Arg	Asp	Gly	Val	Thr	Tyr	Ser	Tyr	Ser	Phe	Phe	His	380	385	390
Phe	Met	Leu	Phe	Leu	Ala	Ser	Leu	Tyr	Ile	Met	Met	Thr	Leu	Thr	395	400	405
Asn	Trp	Ser	Arg	Tyr	Glu	Pro	Ser	Arg	Glu	Met	Lys	Ser	Gln	Trp	410	415	420
Thr	Ala	Val	Trp	Val	Lys	Ile	Ser	Ser	Ser	Trp	Ile	Gly	Ile	Val	425	430	435
Leu	Tyr	Val	Trp	Thr	Leu	Val	Ala	Pro	Leu	Val	Leu	Thr	Asn	Arg	440	445	450

Asp Phe Asp

<210> 74  
 <211> 480  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 48, 163  
 <223> unknown base

<400> 74  
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 cggtgtggag atggggagcg tccctggggc tgtgctccat ggcgagctgg 100  
 ataccatggt tgtgtggaag tgccccgtgt ttgctatgcc gatgctgtcc 150  
 tagtggaac aantccactg taactagatt gatctatgca cttttcttgc 200  
 ttgttgagat atgtgtagct tgtgtaatgt tgataccagg aatggaagaa 250  
 caactgaata agattcctgg attttgtgag aatgagaaaag gtgttgtccc 300  
 ttgtaacatt ttggttggt ataaagctgt atatcgtttg tgctttgggt 350  
 tggctatggt ctatcttctt ctctctttac taatgatcaa agtgaagagt 400

agcagtgatc ctagagctgc agtgcacaat ggattttggt tcttttaaatt 450  
tgctgcagca attgcaatta ttattggggc 480

<210> 75  
<211> 438  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 32, 65, 92, 121, 142, 154, 170, 293, 315, 323  
<223> unknown base

<400> 75  
gttattgtga actttgtgga gatgggaggt cntggggctg tgttccatgg 50  
cgagctggat accangtttg tgtggaagtg ccccggtgtt gntatgccga 100  
tgctgtccta gtggaaacaa ntccactgta attagattga tntatgcact 150  
ttntttgctt gttggagtan gtgtagcttg tgtaatgttg ataccaggaa 200  
tggaagaaca actgaataag attcctggat tttgtgagaa tgagaaaggt 250  
gttgccctt gtaacatttt gggtggctat aaagctgtat atngtttgtg 300  
ctttggtttg gctangttct atnttcttct ctctttacta atgatcaaag 350  
tgaagagtag cagtgatcct agagctgcag tgcacaatgg attttggttt 400  
tttaaatttg ctgcagcaat tgcaattatt attggggc 438

<210> 76  
<211> 473  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 48  
<223> unknown base

<400> 76  
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gagatgggga gcgtccttg gggtgtgctc catggcgagc tggataccat 100  
gtttgtgtgg aagtgtcccg tgtttgcctat gccgatgctg tcctagtggga 150  
aacaactcca ctgtaactag attgatctat gcacttttct tgcttggttg 200  
agtatgtgta gcttgtgtaa tggtgatacc aggaatggaa gaacaactga 250  
ataagattcc tggattttgt gagaatgaga aagggtgttg cccttgtaac 300  
attttggttg gctataaagc tgtatatogt ttgtgctttg gtttggtat 350  
gttctatctt cttctctctt tactaatgat caaagtgaag agtagcagt 400  
atcctagagc tgcagtgcac aatggatttt gggtctttta atttgctgca 450  
gcaattgcaa ttattatttg ggc 473



<210> 77  
<211> 666  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 21, 111  
<223> unknown base

<400> 77  
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caggattgga ngaacaactg aataagattc ctggattttt gtgagaatga 150  
gaaagggtgtt gtccccttgt aacatttttg gttggctata aagctgtata 200  
tcgtttgtgc tttggttgg ctatgttcta tcttcttctc tctttactaa 250  
tgatcaaagt gaagagtagc agtgatccta gagctgcagt gcacaatgga 300  
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cttcattcca gaaggaactt ttacaactgt gtggttttat gtaggcattg 400  
cagggtgcctt ttgtttcatc ctcatacaac tagtcttact tattgatttt 450  
gcacattcat ggaatgaatc gtgggttgaa aaaatggaag aagggaactc 500  
gagatgttgg tatgcagcct tgttatcagc tacagctctg aattatctgc 550  
tgtctttagt tgctatcgtc ctgttctttg tctactacac tcattccagcc 600  
agttgttcag aaaacaaggc gttcatcagt gtcaacatgc tcctctgcgt 650  
tggtgcttct gtaatg 666

<210> 78  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 78  
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<210> 79  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 79  
gtcaacatgc tcctctgc 18

<210> 80  
<211> 26

<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 80  
aatccattgt gcactgcagc tctagg 26

<210> 81  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 81  
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<210> 82  
<211> 54  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 82  
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gcac 54

<210> 83  
<211> 3906  
<212> DNA  
<213> Homo sapiens

<400> 83  
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cgcgaggctt tcggcaaagg cagtcgagtg tttgcagacc ggggagagtc 150  
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<210> 84  
 <211> 867  
 <212> PRT  
 <213> Homo sapiens

<400> 84  
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 35 40 45  
 Ile Ile Leu Val Leu Thr Asp Asp Gln Asp Val Glu Leu Gly Ser  
 50 55 60  
 Met Gln Val Met Asn Lys Thr Arg Arg Ile Met Glu Gln Gly Gly  
 65 70 75  
 Ala His Phe Ile Asn Ala Phe Val Thr Thr Pro Met Cys Cys Pro  
 80 85 90  
 Ser Arg Ser Ser Ile Leu Thr Gly Lys Tyr Val His Asn His Asn  
 95 100 105  
 Thr Tyr Thr Asn Asn Glu Asn Cys Ser Ser Pro Ser Trp Gln Ala  
 110 115 120  
 Gln His Glu Ser Arg Thr Phe Ala Val Tyr Leu Asn Ser Thr Gly  
 125 130 135  
 Tyr Arg Thr Ala Phe Phe Gly Lys Tyr Leu Asn Glu Tyr Asn Gly  
 140 145 150  
 Ser Tyr Val Pro Pro Gly Trp Lys Glu Trp Val Gly Leu Leu Lys  
 155 160 165  
 Asn Ser Arg Phe Tyr Asn Tyr Thr Leu Cys Arg Asn Gly Val Lys  
 170 175 180  
 Glu Lys His Gly Ser Asp Tyr Ser Lys Asp Tyr Leu Thr Asp Leu  
 185 190 195  
 Ile Thr Asn Asp Ser Val Ser Phe Phe Arg Thr Ser Lys Lys Met  
 200 205 210  
 Tyr Pro His Arg Pro Val Leu Met Val Ile Ser His Ala Ala Pro  
 215 220 225  
 His Gly Pro Glu Asp Ser Ala Pro Gln Tyr Ser Arg Leu Phe Pro  
 230 235 240  
 Asn Ala Ser Gln His Ile Thr Pro Ser Tyr Asn Tyr Ala Pro Asn  
 245 250 255

Pro	Asp	Lys	His	Trp	Ile	Met	Arg	Tyr	Thr	Gly	Pro	Met	Lys	Pro	
				260					265					270	
Ile	His	Met	Glu	Phe	Thr	Asn	Met	Leu	Gln	Arg	Lys	Arg	Leu	Gln	
				275					280					285	
Thr	Leu	Met	Ser	Val	Asp	Asp	Ser	Met	Glu	Thr	Ile	Tyr	Asn	Met	
				290					295					300	
Leu	Val	Glu	Thr	Gly	Glu	Leu	Asp	Asn	Thr	Tyr	Ile	Val	Tyr	Thr	
				305					310					315	
Ala	Asp	His	Gly	Tyr	His	Ile	Gly	Gln	Phe	Gly	Leu	Val	Lys	Gly	
				320					325					330	
Lys	Ser	Met	Pro	Tyr	Glu	Phe	Asp	Ile	Arg	Val	Pro	Phe	Tyr	Val	
				335					340					345	
Arg	Gly	Pro	Asn	Val	Glu	Ala	Gly	Cys	Leu	Asn	Pro	His	Ile	Val	
				350					355					360	
Leu	Asn	Ile	Asp	Leu	Ala	Pro	Thr	Ile	Leu	Asp	Ile	Ala	Gly	Leu	
				365					370					375	
Asp	Ile	Pro	Ala	Asp	Met	Asp	Gly	Lys	Ser	Ile	Leu	Lys	Leu	Leu	
				380					385					390	
Asp	Thr	Glu	Arg	Pro	Val	Asn	Arg	Phe	His	Leu	Lys	Lys	Lys	Met	
				395					400					405	
Arg	Val	Trp	Arg	Asp	Ser	Phe	Leu	Val	Glu	Arg	Gly	Lys	Leu	Leu	
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His	Lys	Arg	Asp	Asn	Asp	Lys	Val	Asp	Ala	Gln	Glu	Glu	Asn	Phe	
				425					430					435	
Leu	Pro	Lys	Tyr	Gln	Arg	Val	Lys	Asp	Leu	Cys	Gln	Arg	Ala	Glu	
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Tyr	Gln	Thr	Ala	Cys	Glu	Gln	Leu	Gly	Gln	Lys	Trp	Gln	Cys	Val	
				455					460					465	
Glu	Asp	Ala	Thr	Gly	Lys	Leu	Lys	Leu	His	Lys	Cys	Lys	Gly	Pro	
				470					475					480	
Met	Arg	Leu	Gly	Gly	Ser	Arg	Ala	Leu	Ser	Asn	Leu	Val	Pro	Lys	
				485					490					495	
Tyr	Tyr	Gly	Gln	Gly	Ser	Glu	Ala	Cys	Thr	Cys	Asp	Ser	Gly	Asp	
				500					505					510	
Tyr	Lys	Leu	Ser	Leu	Ala	Gly	Arg	Arg	Lys	Lys	Leu	Phe	Lys	Lys	
				515					520					525	
Lys	Tyr	Lys	Ala	Ser	Tyr	Val	Arg	Ser	Arg	Ser	Ile	Arg	Ser	Val	
				530					535					540	
Ala	Ile	Glu	Val	Asp	Gly	Arg	Val	Tyr	His	Val	Gly	Leu	Gly	Asp	
				545					550					555	
Ala	Ala	Gln	Pro	Arg	Asn	Leu	Thr	Lys	Arg	His	Trp	Pro	Gly	Ala	
				560					565					570	

Pro	Glu	Asp	Gln	Asp	Asp	Lys	Asp	Gly	Gly	Asp	Phe	Ser	Gly	Thr	575	580	585
Gly	Gly	Leu	Pro	Asp	Tyr	Ser	Ala	Ala	Asn	Pro	Ile	Lys	Val	Thr	590	595	600
His	Arg	Cys	Tyr	Ile	Leu	Glu	Asn	Asp	Thr	Val	Gln	Cys	Asp	Leu	605	610	615
Asp	Leu	Tyr	Lys	Ser	Leu	Gln	Ala	Trp	Lys	Asp	His	Lys	Leu	His	620	625	630
Ile	Asp	His	Glu	Ile	Glu	Thr	Leu	Gln	Asn	Lys	Ile	Lys	Asn	Leu	635	640	645
Arg	Glu	Val	Arg	Gly	His	Leu	Lys	Lys	Lys	Arg	Pro	Glu	Glu	Cys	650	655	660
Asp	Cys	His	Lys	Ile	Ser	Tyr	His	Thr	Gln	His	Lys	Gly	Arg	Leu	665	670	675
Lys	His	Arg	Gly	Ser	Ser	Leu	His	Pro	Phe	Arg	Lys	Gly	Leu	Gln	680	685	690
Glu	Lys	Asp	Lys	Val	Trp	Leu	Leu	Arg	Glu	Gln	Lys	Arg	Lys	Lys	695	700	705
Lys	Leu	Arg	Lys	Leu	Leu	Lys	Arg	Leu	Gln	Asn	Asn	Asp	Thr	Cys	710	715	720
Ser	Met	Pro	Gly	Leu	Thr	Cys	Phe	Thr	His	Asp	Asn	Gln	His	Trp	725	730	735
Gln	Thr	Ala	Pro	Phe	Trp	Thr	Leu	Gly	Pro	Phe	Cys	Ala	Cys	Thr	740	745	750
Ser	Ala	Asn	Asn	Asn	Thr	Tyr	Trp	Cys	Met	Arg	Thr	Ile	Asn	Glu	755	760	765
Thr	His	Asn	Phe	Leu	Phe	Cys	Glu	Phe	Ala	Thr	Gly	Phe	Leu	Glu	770	775	780
Tyr	Phe	Asp	Leu	Asn	Thr	Asp	Pro	Tyr	Gln	Leu	Met	Asn	Ala	Val	785	790	795
Asn	Thr	Leu	Asp	Arg	Asp	Val	Leu	Asn	Gln	Leu	His	Val	Gln	Leu	800	805	810
Met	Glu	Leu	Arg	Ser	Cys	Lys	Gly	Tyr	Lys	Gln	Cys	Asn	Pro	Arg	815	820	825
Thr	Arg	Asn	Met	Asp	Leu	Asp	Gly	Gly	Ser	Tyr	Glu	Gln	Tyr	Arg	830	835	840
Gln	Phe	Gln	Arg	Arg	Lys	Trp	Pro	Glu	Met	Lys	Arg	Pro	Ser	Ser	845	850	855
Lys	Ser	Leu	Gly	Gln	Leu	Trp	Glu	Gly	Trp	Glu	Gly				860	865	

<210> 85  
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 <212> DNA

<213> Artificial Sequence  
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 <223> Synthetic oligonucleotide probe  
 <400> 85  
 gaagccggct gtctgaatc 19  
 <210> 86  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence  
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 <223> Synthetic oligonucleotide probe  
 <400> 86  
 ggccagctat ctccgcag 18  
 <210> 87  
 <211> 18  
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 <213> Artificial Sequence  
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 <223> Synthetic oligonucleotide probe  
 <400> 87  
 aagggcctgc aagagaag 18  
 <210> 88  
 <211> 18  
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 <223> Synthetic oligonucleotide probe  
 <400> 88  
 cactgggaca actgtggg 18  
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 <211> 18  
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 <400> 89  
 cagaggcaac gtggagag 18  
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 <223> Synthetic oligonucleotide probe  
 <400> 90  
 aagtattgtc atacagtgtt c 21



<210> 91  
<211> 24  
<212> DNA  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 91  
tagtacttgg gcacgaggtt ggag 24

<210> 92  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 92  
tcataccaac tgctgggtcat tggc 24

<210> 93  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 93  
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<210> 94  
<211> 971  
<212> DNA  
<213> Homo sapiens

<400> 94  
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aaggagtgag gagctgctgg gcagagaggg actgtccggc tcccagatgc 100  
tgggcctcct ggggagcaca gccctcgtgg gatggatcac aggtgctgct 150  
gtggcggtcc tgetgctgct gctgctgctg gccacctgcc ttttccacgg 200  
acggcaggac tgtgacgtgg agaggaaccg tacagctgca gggggaaacc 250  
gagtcgcgcg ggcccagcct tggcccttcc ggcggcgggg ccacctggga 300  
atctttcacc atcacctgca tcctggccac gtatctcatg tgccgaatgt 350  
gggcctccac caccaccacc acccccgcca caccctcac cacctccacc 400  
accaccacca cccccaccgc caccatcccc gccacgctcg ctgaggctgc 450  
tgtcgccggt gcctgtggac agcagctgcc cctgccctcc catctgttcc 500  
caggacaagt ggaccccatg tttccatgtg gaaggatgca tctctgggg 550  
gaacgagggg aacaatagac tggggccttg tccagctgca tttgcatggc 600

atgccccagt gtactatggc agcagagaat ggaggaacac tgggtctgca 650  
 gtgctgaagg gtttggggag tggagagcaa ggggtgctctt tcggggctgg 700  
 acagcccgtc ttgtgacagt gactcccagt gagccccaga aatgacaagc 750  
 gtgtcttggc agagccagca cacaagtgga tgtgaagtgc ccgtcttgac 800  
 ctctcatca ggctgctgca ggctcttggc gggcagggca ctgggagagg 850  
 ccctgagaat gtccttttgg tttggagaag gcagtgtgag gctgcacagt 900  
 caattcatcg gtgccttagt ccaagaaaat aaaaaccact aagaagcttt 950  
 aaaaaaaaaa aaaaaaaaaa a 971

<210> 95  
 <211> 115  
 <212> PRT  
 <213> Homo sapiens

<400> 95  
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 Gly Ala Ala Val Ala Val Leu Leu Leu Leu Leu Leu Ala Thr  
 20 25 30  
 Cys Leu Phe His Gly Arg Gln Asp Cys Asp Val Glu Arg Asn Arg  
 35 40 45  
 Thr Ala Ala Gly Gly Asn Arg Val Arg Arg Ala Gln Pro Trp Pro  
 50 55 60  
 Phe Arg Arg Arg Gly His Leu Gly Ile Phe His His His Arg His  
 65 70 75  
 Pro Gly His Val Ser His Val Pro Asn Val Gly Leu His His His  
 80 85 90  
 His His Pro Arg His Thr Pro His His Leu His His His His His  
 95 100 105  
 Pro His Arg His His Pro Arg His Ala Arg  
 110 115

<210> 96  
 <211> 1312  
 <212> DNA  
 <213> Homo sapiens

<400> 96  
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 gctgacgctg ctggcctttg ccgggtactc agggctactg gctgggggtg 150  
 aagtgagtgc tgggtcacc cccatccgca acgtcactgt ggcctacaag 200  
 ttccacatgg ggctctatgg tgagactggg cggtctttca ctgagagctg 250  
 cagcatctct cccaagctcc gctccatcgc tgtctactat gacaaccccc 300

acatggtgcc ccctgataag tgccgatgtg ccgtgggcag catcctgagt 350  
 gaaggtgagg aatcgccctc ccctgagctc atcgacctct accagaaatt 400  
 tggcttcaag gtgtttctct tcccggcacc cagccatgtg gtgacagcca 450  
 ccttcccccta caccaccatt ctgtccatct ggctggctac ccgccgtgtc 500  
 catcctgcct tggacaccta catcaaggag cggaagctgt gtgcctatcc 550  
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 cacggcaggg agacttctat gtgcctgaga tgaaggagac agagtggaaa 650  
 tggcgggggc ttgtggaggg cattgacacc caggtggatg gcacaggagc 700  
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 gccgggagac ttcagctgcc acaactgtcac ctggggcgag cagccgtggc 800  
 tgggatgacg gtgacacccg cagcgagcac agctacagcg agtcaggtgc 850  
 cagcggctcc tcttttgagg agctggactt ggagggcgag gggcccttag 900  
 gggagtcacg gctggaccct gggactgagc cctgggggac taccaagtgg 950  
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 caccctcctg cagtgcagtt gctgaggaac tgagcagact ctccagcaga 1050  
 ctctccagcc ctcttcctcc ttcctctggg ggaggagggg ttcctgaggg 1100  
 acctgacttc cctgctcca ggcctcttgc taagccttct cctcactgcc 1150  
 ctttaggctc ccagggccag aggagccagg gactattttc tgcaccagcc 1200  
 cccagggctg ccgccctgt tgtgtctttt tttcagactc acagtggagc 1250  
 ttccaggacc cagaataaag ccaatgattt acttgtttca cctggaaaaa 1300  
 aaaaaaaaaa aa 1312

<210> 97  
 <211> 313  
 <212> PRT  
 <213> Homo sapiens

<400> 97  
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 20 25 30  
 Leu Ala Gly Val Glu Val Ser Ala Gly Ser Pro Pro Ile Arg Asn  
 35 40 45  
 Val Thr Val Ala Tyr Lys Phe His Met Gly Leu Tyr Gly Glu Thr  
 50 55 60  
 Gly Arg Leu Phe Thr Glu Ser Cys Ser Ile Ser Pro Lys Leu Arg  
 65 70 75

Ser	Ile	Ala	Val	Tyr	Tyr	Asp	Asn	Pro	His	Met	Val	Pro	Pro	Asp	
				80					85					90	
Lys	Cys	Arg	Cys	Ala	Val	Gly	Ser	Ile	Leu	Ser	Glu	Gly	Glu	Glu	
				95					100					105	
Ser	Pro	Ser	Pro	Glu	Leu	Ile	Asp	Leu	Tyr	Gln	Lys	Phe	Gly	Phe	
				110					115					120	
Lys	Val	Phe	Ser	Phe	Pro	Ala	Pro	Ser	His	Val	Val	Thr	Ala	Thr	
				125					130					135	
Phe	Pro	Tyr	Thr	Thr	Ile	Leu	Ser	Ile	Trp	Leu	Ala	Thr	Arg	Arg	
				140					145					150	
Val	His	Pro	Ala	Leu	Asp	Thr	Tyr	Ile	Lys	Glu	Arg	Lys	Leu	Cys	
				155					160					165	
Ala	Tyr	Pro	Arg	Leu	Glu	Ile	Tyr	Gln	Glu	Asp	Gln	Ile	His	Phe	
				170					175					180	
Met	Cys	Pro	Leu	Ala	Arg	Gln	Gly	Asp	Phe	Tyr	Val	Pro	Glu	Met	
				185					190					195	
Lys	Glu	Thr	Glu	Trp	Lys	Trp	Arg	Gly	Leu	Val	Glu	Ala	Ile	Asp	
				200					205					210	
Thr	Gln	Val	Asp	Gly	Thr	Gly	Ala	Asp	Thr	Met	Ser	Asp	Thr	Ser	
				215					220					225	
Ser	Val	Ser	Leu	Glu	Val	Ser	Pro	Gly	Ser	Arg	Glu	Thr	Ser	Ala	
				230					235					240	
Ala	Thr	Leu	Ser	Pro	Gly	Ala	Ser	Ser	Arg	Gly	Trp	Asp	Asp	Gly	
				245					250					255	
Asp	Thr	Arg	Ser	Glu	His	Ser	Tyr	Ser	Glu	Ser	Gly	Ala	Ser	Gly	
				260					265					270	
Ser	Ser	Phe	Glu	Glu	Leu	Asp	Leu	Glu	Gly	Glu	Gly	Pro	Leu	Gly	
				275					280					285	
Glu	Ser	Arg	Leu	Asp	Pro	Gly	Thr	Glu	Pro	Leu	Gly	Thr	Thr	Lys	
				290					295					300	
Trp	Leu	Trp	Glu	Pro	Thr	Ala	Pro	Glu	Lys	Gly	Lys	Glu			
				305					310						

<210> 98

<211> 725

<212> DNA

<213> Homo sapiens

<400> 98

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ctgaggctgg gctcgaaacc gaaagtcccg tccggaccct ccaagtggag 200

accctggtgg agccccaga accatgtgcc gagcccgctg cttttggaga 250

cacgcttcac atacactaca cggaagcctt ggtagatgga cgtattattg 300  
acacctccct gaccagagac cctctgggta tagaacttgg ccaaaagcag 350  
gtgattccag gtctggagca gagtcttctc gacatgtgtg tgggagagaa 400  
gcgaagggca atcattcctt ctacttggc ctatggaaaa cggggatttc 450  
caccatctgt cccagcggat gcagtgggtgc agtatgacgt ggagctgatt 500  
gcactaatcc gagccaacta ctggctaaag ctggtgaagg gcattttgcc 550  
tctggtaggg atggccatgg tgccagccct cctgggcctc attgggtatc 600  
acctatacag aaaggccaat agacccaaag tctccaaaaa gaagctcaag 650  
gaagagaaac gaaacaagag caaaaagaaa taataaataa taaattttaa 700  
aaaacttaaa aaaaaaaaaa aaaaa 725

<210> 99  
<211> 201  
<212> PRT  
<213> Homo sapiens

<400> 99  
Met Thr Leu Arg Pro Ser Leu Leu Pro Leu His Leu Leu Leu Leu  
1 5 10 15  
Leu Leu Leu Ser Ala Ala Val Cys Arg Ala Glu Ala Gly Leu Glu  
20 25 30  
Thr Glu Ser Pro Val Arg Thr Leu Gln Val Glu Thr Leu Val Glu  
35 40 45  
Pro Pro Glu Pro Cys Ala Glu Pro Ala Ala Phe Gly Asp Thr Leu  
50 55 60  
His Ile His Tyr Thr Gly Ser Leu Val Asp Gly Arg Ile Ile Asp  
65 70 75  
Thr Ser Leu Thr Arg Asp Pro Leu Val Ile Glu Leu Gly Gln Lys  
80 85 90  
Gln Val Ile Pro Gly Leu Glu Gln Ser Leu Leu Asp Met Cys Val  
95 100 105  
Gly Glu Lys Arg Arg Ala Ile Ile Pro Ser His Leu Ala Tyr Gly  
110 115 120  
Lys Arg Gly Phe Pro Pro Ser Val Pro Ala Asp Ala Val Val Gln  
125 130 135  
Tyr Asp Val Glu Leu Ile Ala Leu Ile Arg Ala Asn Tyr Trp Leu  
140 145 150  
Lys Leu Val Lys Gly Ile Leu Pro Leu Val Gly Met Ala Met Val  
155 160 165  
Pro Ala Leu Leu Gly Leu Ile Gly Tyr His Leu Tyr Arg Lys Ala  
170 175 180  
Asn Arg Pro Lys Val Ser Lys Lys Lys Leu Lys Glu Glu Lys Arg

185

190

195

Asn Lys Ser Lys Lys Lys  
200

<210> 100  
<211> 705  
<212> DNA  
<213> Homo sapiens

<400> 100  
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cgctccatct gctgctgctg ctgctgctca gtgcggcggt gtgccgggct 150  
gaggctgggc tcgaaaccga aagtcccgtc cggaccctcc aagtggagac 200  
cctgggtggag cccccaagaac catgtgccga gcccgctgct tttggagaca 250  
cgcttcacat aactacacg ggaagcttgg tagatggacg tattattgac 300  
acctccctga ccagagaccc tctggttata gaacttggcc aaaagcaggt 350  
gattccaggt ctggagcaga gtcttctcga catgtgtgtg ggagagaagc 400  
gaagggcaat cattccttct cacttggcct atggaaaacg gggatttcca 450  
ccatctgtcc cagcggatgc agtgggtgcag tatgacgtgg agctgattgc 500  
actaatccga gccaaactact ggctaaagct ggtgaagggc attttgcctc 550  
tggtagggat ggccatggtg ccacctcctt gggcctcatt gggtatcacc 600  
tatacagaaa ggccaataga cccaaagtct ccaaaaagaa gctcaaggaa 650  
gagaaacgaa acaagagcaa aaagaaataa taaataataa attttaaaaa 700  
actta 705

<210> 101  
<211> 543  
<212> DNA  
<213> Homo sapiens

<400> 101  
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gaaccatgtg ccgagcccg cgtcttttga gacacgcttc acatacacta 100  
cacgggaagc ttggtagatg gacgtattat tgacacctcc ctgaccagag 150  
accctctggt tatagaactt ggccaaaagc aggtgattcc aggtctggag 200  
cagagtcttc tcgacatgtg tgtgggagag aagcgaaggg caatcattcc 250  
ttctcacttg gcctatggaa aacggggatt tccaccatct gtcccagcgg 300  
atgcagtggg gcagtatgac gtggagctga ttgcactaat ccgagccaac 350  
tactggctaa agctggtgaa gggcattttg cctctggtag ggatggccat 400

ggtgccagcc ctcttgggcc tcattgggta tcacctatac agaaaggcca 450  
 atagacccaa agtctccaaa aagaagctca aggaagagaa acgaaacaag 500  
 agcaaaaaga aataataaat aataaatttt aaaaaactta aaa 543

<210> 102  
 <211> 1316  
 <212> DNA  
 <213> Homo sapiens

<400> 102  
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 ccactgcacg acggggcttg actgacctga aaaaaatgtc tggatttcta 150  
 gagggcttga gatgctcaga atgcattgac tggggggaaa agcgcaatac 200  
 tattgcttcc attgctgctg gtgtactatt ttttacaggc tgggtggatta 250  
 tcatagatgc agctgttatt tatcccacca tgaaagattt caaccactca 300  
 taccatgcct gtggtgttat agcaaccata gccttcttaa tgattaatgc 350  
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 gtcaaacagg tgctcgcatc ttgcttttcg ttggtttcat gttggccttt 450  
 ggatctctga ttgcatctat gtggattcct tttggagggt atgttgctaa 500  
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 tcatcttttt tggagggtg gtttttaagt ttggcgcac tgaagactta 600  
 tggcagtga cacaatctgat ttcccacagc acaacagccc tgcattgggt 650  
 tgtttgtttt tttactgctc actcccaacc ttttgtaatg ccattttcta 700  
 aacttatttc tgagtgtagt ctacagctta agttgtgtaa tactaaaatc 750  
 acgagaacac ctaaacaaca accaaaaatc tattgtggta tgcacttgat 800  
 taacttataa aatgttagag gaaactttca catgaataat ttttgtcaaa 850  
 ttttatcatg gtataatttg taaaaataaa aagaaattac aaaagaaatt 900  
 atggatttgt caatgtaagt atttgtcata tctgagggtc aaaaccacaa 950  
 tgaaagtgct ctgaagattt aatgtgttta ttcaaattgt gtctcttctg 1000  
 tgtcaaatgt taaatgaaat ataaacattt tttagttttt aaaatatttc 1050  
 gtgggtcaaaa ttcttcctca ctataattgg tatttacttt taccaaaaat 1100  
 tctgtgaaca tgtaatgtaa ctggcttttg aggggtctcc aaggggtgag 1150  
 tggacgtgtt ggaagagaga agcaccatgg tccagccacc aggctccctg 1200  
 tgtcccttcc atgggaaggt cttccgctgt gcctctcatt ccaagggcag 1250  
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tccacatcca ccaactg 1316

<210> 103  
<211> 157  
<212> PRT  
<213> Homo sapiens

<400> 103  
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Trp Gly Glu Lys Arg Asn Thr Ile Ala Ser Ile Ala Ala Gly Val  
20 25 30  
Leu Phe Phe Thr Gly Trp Trp Ile Ile Ile Asp Ala Ala Val Ile  
35 40 45  
Tyr Pro Thr Met Lys Asp Phe Asn His Ser Tyr His Ala Cys Gly  
50 55 60  
Val Ile Ala Thr Ile Ala Phe Leu Met Ile Asn Ala Val Ser Asn  
65 70 75  
Gly Gln Val Arg Gly Asp Ser Tyr Ser Glu Gly Cys Leu Gly Gln  
80 85 90  
Thr Gly Ala Arg Ile Trp Leu Phe Val Gly Phe Met Leu Ala Phe  
95 100 105  
Gly Ser Leu Ile Ala Ser Met Trp Ile Leu Phe Gly Gly Tyr Val  
110 115 120  
Ala Lys Glu Lys Asp Ile Val Tyr Pro Gly Ile Ala Val Phe Phe  
125 130 135  
Gln Asn Ala Phe Ile Phe Phe Gly Gly Leu Val Phe Lys Phe Gly  
140 145 150  
Arg Thr Glu Asp Leu Trp Gln  
155

<210> 104  
<211> 545  
<212> DNA  
<213> Homo sapiens

<400> 104  
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tggatttcta gagggcttga gatgctcaga atgcattgac tggggggaaa 150  
agcgcaatac tattgcttcc attgctgctg gtgtactatt ttttacaggc 200  
tggttgatta tcatagatgc agctgttatt tatccacca tgaaagattt 250  
caaccactca taccatgcct gtggtgttat agcaaccata gccttcctaa 300  
tgattaatgc agtatcgaat ggacaagtcc gaggtgatag ttacagtga 350  
ggttgtctgg gtcaaacagg tgctcgcat tggcttttcg ttggtttcat 400



gttggccttt ggatctctga ttgcatctat gtggattctt tttggagggt 450  
atgttgctaa agaaaaagac atagtataacc ctggaattgc tgtatttttc 500  
cagaatgcct tcatcttttt tggagggctg gtttttaagt ttggc 545

<210> 105  
<211> 490  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 31, 39, 108, 145, 179, 219, 412, 479  
<223> unknown base

<400> 105  
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agaatgcatg actgggggaa aagcgcaaat actattgctt ccattgctgc 100  
tgggtgtaata ttttttacag gctgggtggat tatcatagat gcagntgtta 150  
tttatccac catgaaagat ttcaaccant cataccatgc ctgtgggtgtt 200  
atagcaacca tagccttcnt aatgattaat gcagtatcga atggacaagt 250  
ccgaggtgat agttacagtg aaggttggtt ggggtcaaaca ggtgctcgca 300  
tttggctttt cgttgggttc atgttggcct ttggatctct gattgcatct 350  
atgtggattc tttttggagg ttatgttgct aaagaaaaag acatagtata 400  
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<210> 106  
<211> 466  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 26, 38, 81, 115, 207, 329, 380, 446, 449  
<223> unknown base

<400> 106  
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ggaaaagcgc aatantattg ctttccattg ctgctgggtgt actatttttt 150  
acagggtggt ggattatcat agatgcagct gttattttatc ccaccatgaa 200  
agatttnaac cactcatacc atgcctgtgg tgttatagca accatagcct 250  
tcctaataatg taatgcagta tcgaatggac aagtcagagg tgatagttac 300  
agtgaagggt gtttgggtca aacagggtgnt cgcatttggc ttttcgttgg 350  
tttcatgttg gcctttggat ttctgattgn attotatgcg gattcttctt 400

0099599 41501

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atTTTTccag aatgcc 466

<210> 107

<211> 377

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 52, 67, 70, 78, 105, 144, 150, 209, 266, 268, 282, 310, 331, 356

<223> unknown base

<400> 107

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antattgctt ccattgntgn tgggtgnta tttttttaca ggctgggtgga 100

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tcataccatg cctgtggtgt tatagcaacc atagccttcc taatgattaa 200

tgcagtatng aatggacaag tccgaggtga tagttacagt gaaggttggt 250

tgggtcaaac aggtgntngc atttggcttt tngttgggtt catgttggcc 300

tttggatctn tgattgcatt tatgtggatt ntttttggag gttatgttgc 350

taaagnaaaa gacatagtat accctgt 377

<210> 108

<211> 552

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 12, 25, 65, 130, 437, 537

<223> unknown base

<400> 108

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ggactgacct gaaaaaatg tttggatttn tagagggctt gagatgctca 150

gaatgcattg actgggggga aaagcgcaat actattgctt ccattgctgc 200

tgggtgtacta ttttttacag gctggtggat tatcatagat gcagctgtta 250

tttatccac catgaaagat ttcaaccact cataccatgc ctgtgggtgtt 300

atagcaacca tagccttctt aatgattaat gcagtatcga atggacaagt 350

ccgaggtgat agttacagtg aaggttgtct ggggtcaaaca ggtgctcgca 400

tttggctttt cgttggtttc atgttggcct ttggatntct gattgcatct 450

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<210> 109  
<211> 23  
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<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 109  
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<210> 110  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 110  
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<210> 111  
<211> 46  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 111  
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<210> 112  
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<212> DNA  
<213> Homo sapiens

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ccgaatcctt tctccgaaga tgtcaaacgg cccccagcgc ccctggtaac 150  
tgacaaggag gccaggaaga aggttctcaa acaagctttt tcagccaacc 200  
aagtgccgga gaagctggat gtggtggtaa ttggcagtgg ctttgggggc 250  
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 aaaa 3004

<210> 113  
 <211> 610  
 <212> PRT  
 <213> Homo sapiens

<400> 113  
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 Asn Pro Phe Ser Glu Asp Val Lys Arg Pro Pro Ala Pro Leu Val  
 35 40 45  
 Thr Asp Lys Glu Ala Arg Lys Lys Val Leu Lys Gln Ala Phe Ser  
 50 55 60  
 Ala Asn Gln Val Pro Glu Lys Leu Asp Val Val Val Ile Gly Ser  
 65 70 75  
 Gly Phe Gly Gly Leu Ala Ala Ala Ala Ile Leu Ala Lys Ala Gly  
 80 85 90  
 Lys Arg Val Leu Val Leu Glu Gln His Thr Lys Ala Gly Gly Cys  
 95 100 105

Cys	His	Thr	Phe	Gly	Lys	Asn	Gly	Leu	Glu	Phe	Asp	Thr	Gly	Ile	
				110					115					120	
His	Tyr	Ile	Gly	Arg	Met	Glu	Glu	Gly	Ser	Ile	Gly	Arg	Phe	Ile	
				125					130					135	
Leu	Asp	Gln	Ile	Thr	Glu	Gly	Gln	Leu	Asp	Trp	Ala	Pro	Leu	Ser	
				140					145					150	
Ser	Pro	Phe	Asp	Ile	Met	Val	Leu	Glu	Gly	Pro	Asn	Gly	Arg	Lys	
				155					160					165	
Glu	Tyr	Pro	Met	Tyr	Ser	Gly	Glu	Lys	Ala	Tyr	Ile	Gln	Gly	Leu	
				170					175					180	
Lys	Glu	Lys	Phe	Pro	Gln	Glu	Glu	Ala	Ile	Ile	Asp	Lys	Tyr	Ile	
				185					190					195	
Lys	Leu	Val	Lys	Val	Val	Ser	Ser	Gly	Ala	Pro	His	Ala	Ile	Leu	
				200					205					210	
Leu	Lys	Phe	Leu	Pro	Leu	Pro	Val	Val	Gln	Leu	Leu	Asp	Arg	Cys	
				215					220					225	
Gly	Leu	Leu	Thr	Arg	Phe	Ser	Pro	Phe	Leu	Gln	Ala	Ser	Thr	Gln	
				230					235					240	
Ser	Leu	Ala	Glu	Val	Leu	Gln	Gln	Leu	Gly	Ala	Ser	Ser	Glu	Leu	
				245					250					255	
Gln	Ala	Val	Leu	Ser	Tyr	Ile	Phe	Pro	Thr	Tyr	Gly	Val	Thr	Pro	
				260					265					270	
Asn	His	Ser	Ala	Phe	Ser	Met	His	Ala	Leu	Leu	Val	Asn	His	Tyr	
				275					280					285	
Met	Lys	Gly	Gly	Phe	Tyr	Pro	Arg	Gly	Gly	Ser	Ser	Glu	Ile	Ala	
				290					295					300	
Phe	His	Thr	Ile	Pro	Val	Ile	Gln	Arg	Ala	Gly	Gly	Ala	Val	Leu	
				305					310					315	
Thr	Lys	Ala	Thr	Val	Gln	Ser	Val	Leu	Leu	Asp	Ser	Ala	Gly	Lys	
				320					325					330	
Ala	Cys	Gly	Val	Ser	Val	Lys	Lys	Gly	His	Glu	Leu	Val	Asn	Ile	
				335					340					345	
Tyr	Cys	Pro	Ile	Val	Val	Ser	Asn	Ala	Gly	Leu	Phe	Asn	Thr	Tyr	
				350					355					360	
Glu	His	Leu	Leu	Pro	Gly	Asn	Ala	Arg	Cys	Leu	Pro	Gly	Val	Lys	
				365					370					375	
Gln	Gln	Leu	Gly	Thr	Val	Arg	Pro	Gly	Leu	Gly	Met	Thr	Ser	Val	
				380					385					390	
Phe	Ile	Cys	Leu	Arg	Gly	Thr	Lys	Glu	Asp	Leu	His	Leu	Pro	Ser	
				395					400					405	
Thr	Asn	Tyr	Tyr	Val	Tyr	Tyr	Asp	Thr	Asp	Met	Asp	Gln	Ala	Met	
				410					415					420	

Glu Arg Tyr Val	Ser Met Pro Arg Glu	Glu Ala Ala Glu His	Ile
	425	430	435
Pro Leu Leu Phe	Phe Ala Phe Pro Ser	Ala Lys Asp Pro Thr	Trp
	440	445	450
Glu Asp Arg Phe	Pro Gly Arg Ser Thr	Met Ile Met Leu Ile	Pro
	455	460	465
Thr Ala Tyr Glu	Trp Phe Glu Glu Trp	Gln Ala Glu Leu Lys	Gly
	470	475	480
Lys Arg Gly Ser	Asp Tyr Glu Thr Phe	Lys Asn Ser Phe Val	Glu
	485	490	495
Ala Ser Met Ser	Val Val Leu Lys Leu	Phe Pro Gln Leu Glu	Gly
	500	505	510
Lys Val Glu Ser	Val Thr Ala Gly Ser	Pro Leu Thr Asn Gln	Phe
	515	520	525
Tyr Leu Ala Ala	Pro Arg Gly Ala Cys	Tyr Gly Ala Asp His	Asp
	530	535	540
Leu Gly Arg Leu	His Pro Cys Val Met	Ala Ser Leu Arg Ala	Gln
	545	550	555
Ser Pro Ile Pro	Asn Leu Tyr Leu Thr	Gly Gln Asp Ile Phe	Thr
	560	565	570
Cys Gly Leu Val	Gly Ala Leu Gln Gly	Ala Leu Leu Cys Ser	Ser
	575	580	585
Ala Ile Leu Lys	Arg Asn Leu Tyr Ser	Asp Leu Lys Asn Leu	Asp
	590	595	600
Ser Arg Ile Arg	Ala Gln Lys Lys Lys	Asn	
	605	610	

<210> 114  
 <211> 1701  
 <212> DNA  
 <213> Homo sapiens

<400> 114  
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 actttgacat cagatgagtc agtaaaggac catactactg caggcagagt 250  
 agttgctggt caaatatttc ttgattcaga agaatctgaa ttagaatcct 300  
 ctattcaaga agaggaagac agcctcaaga gccaagaggg ggaaagtgtc 350  
 acagaagata tcagctttct agagtctcca aatccagaaa acaaggacta 400  
 tgaagagcca aagaaagtac ggaaaccagc ttgaccgcc attgaaggca 450

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atttttaata aaattatgtc taagattaaa aaaaaaaaaa aaaaaaaaaa 1650  
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a 1701

<210> 115  
<211> 301  
<212> PRT  
<213> Homo sapiens

<400> 115  
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Leu Ser Leu Ala Ser Ala Ser Ser Asp Glu Glu Gly Ser Gln Asp  
20 25 30



Glu	Ser	Leu	Asp	Ser	Lys	Thr	Thr	Leu	Thr	Ser	Asp	Glu	Ser	Val	35	40	45
Lys	Asp	His	Thr	Thr	Ala	Gly	Arg	Val	Val	Ala	Gly	Gln	Ile	Phe	50	55	60
Leu	Asp	Ser	Glu	Glu	Ser	Glu	Leu	Glu	Ser	Ser	Ile	Gln	Glu	Glu	65	70	75
Glu	Asp	Ser	Leu	Lys	Ser	Gln	Glu	Gly	Glu	Ser	Val	Thr	Glu	Asp	80	85	90
Ile	Ser	Phe	Leu	Glu	Ser	Pro	Asn	Pro	Glu	Asn	Lys	Asp	Tyr	Glu	95	100	105
Glu	Pro	Lys	Lys	Val	Arg	Lys	Pro	Ala	Leu	Thr	Ala	Ile	Glu	Gly	110	115	120
Thr	Ala	His	Gly	Glu	Pro	Cys	His	Phe	Pro	Phe	Leu	Phe	Leu	Asp	125	130	135
Lys	Glu	Tyr	Asp	Glu	Cys	Thr	Ser	Asp	Gly	Arg	Glu	Asp	Gly	Arg	140	145	150
Leu	Trp	Cys	Ala	Thr	Thr	Tyr	Asp	Tyr	Lys	Ala	Asp	Glu	Lys	Trp	155	160	165
Gly	Phe	Cys	Glu	Thr	Glu	Glu	Glu	Ala	Ala	Lys	Arg	Arg	Gln	Met	170	175	180
Gln	Glu	Ala	Glu	Met	Met	Tyr	Gln	Thr	Gly	Met	Lys	Ile	Leu	Asn	185	190	195
Gly	Ser	Asn	Lys	Lys	Ser	Gln	Lys	Arg	Glu	Ala	Tyr	Arg	Tyr	Leu	200	205	210
Gln	Lys	Ala	Ala	Ser	Met	Asn	His	Thr	Lys	Ala	Leu	Glu	Arg	Val	215	220	225
Ser	Tyr	Ala	Leu	Leu	Phe	Gly	Asp	Tyr	Leu	Pro	Gln	Asn	Ile	Gln	230	235	240
Ala	Ala	Arg	Glu	Met	Phe	Glu	Lys	Leu	Thr	Glu	Glu	Gly	Ser	Pro	245	250	255
Lys	Gly	Gln	Thr	Ala	Leu	Gly	Phe	Leu	Tyr	Ala	Ser	Gly	Leu	Gly	260	265	270
Val	Asn	Ser	Ser	Gln	Ala	Lys	Ala	Leu	Val	Tyr	Tyr	Thr	Phe	Gly	275	280	285
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Leu

<210> 116  
 <211> 584  
 <212> DNA  
 <213> Homo sapiens

<400> 116

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 agctggatgc actgctggtc tcccaggcc aagtggctca actctcctgc 200  
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 aaaatgggtt aataatattc aacatgtcaa caac 584

<210> 117  
 <211> 123  
 <212> PRT  
 <213> Homo sapiens

<400> 117  
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 Phe Pro Gly Gln Val Ala Gln Leu Ser Cys Thr Leu Ser Pro Gln  
 35 40 45  
 His Val Thr Ile Arg Asp Tyr Gly Val Ser Trp Tyr Gln Gln Arg  
 50 55 60  
 Ala Gly Ser Ala Pro Arg Tyr Leu Leu Tyr Tyr Arg Ser Glu Glu  
 65 70 75  
 Asp His His Arg Pro Ala Asp Ile Pro Asp Arg Phe Ser Ala Ala  
 80 85 90  
 Lys Asp Glu Ala His Asn Ala Cys Val Leu Thr Ile Ser Pro Val  
 95 100 105  
 Gln Pro Glu Asp Asp Ala Asp Tyr Tyr Cys Ser Val Gly Tyr Gly  
 110 115 120  
 Phe Ser Pro

<210> 118  
 <211> 3402  
 <212> DNA  
 <213> Homo sapiens

<400> 118

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 gccttccac cgccgcccgc cgcccgaggc ccccaaaga tggcgacaa 250  
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 cgcaccatcc acagcggtg gagccgcttc cgcgtgctgc cgcaggggct 400  
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 ggtcaagag gaccccgcca gccagcagtg ggcacgaccg cgcttcacac 600  
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 gtgcggtca agtgcgtggc cagcgggcac cctcgggccg acatcacgtg 700  
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 aaatacacct gccgcgtgtc gaaccgcgcg ggcgccatca acgccaccta 850  
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 tcctacctca ataagctgct catcacccgt gcccgccagg acgatgcggg 1150  
 catgtacatc tgccttgggc ccaacaccat gggctacagc ttccgcagcg 1200  
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 tcctcgtcct cggccaactag cctgcgcgtg ccgctgggtca tcggcatccc 1300  
 agccggcgct gtcttcatcc tgggcaccct gtcctgttg ctttgccagg 1350  
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 cgcccgccgg ggacggcccg cgaccgcagc ggagacaagg acctccctc 1450  
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 ccacccccca cccactgtc gtggtggccc cagatctctg taattttatg 3350  
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 aa 3402

<210> 119  
 <211> 504  
 <212> PRT  
 <213> Homo sapiens

<400> 119  
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 Met Ala Asp Lys Val Val Pro Arg Gln Val Ala Arg Leu Gly Arg  
 35 40 45  
 Thr Val Arg Leu Gln Cys Pro Val Glu Gly Asp Pro Pro Pro Leu  
 50 55 60  
 Thr Met Trp Thr Lys Asp Gly Arg Thr Ile His Ser Gly Trp Ser  
 65 70 75  
 Arg Phe Arg Val Leu Pro Gln Gly Leu Lys Val Lys Gln Val Glu  
 80 85 90  
 Arg Glu Asp Ala Gly Val Tyr Val Cys Lys Ala Thr Asn Gly Phe  
 95 100 105  
 Gly Ser Leu Ser Val Asn Tyr Thr Leu Val Val Leu Asp Asp Ile  
 110 115 120  
 Ser Pro Gly Lys Glu Ser Leu Gly Pro Asp Ser Ser Ser Gly Gly  
 125 130 135  
 Gln Glu Asp Pro Ala Ser Gln Gln Trp Ala Arg Pro Arg Phe Thr  
 140 145 150  
 Gln Pro Ser Lys Met Arg Arg Arg Val Ile Ala Arg Pro Val Gly  
 155 160 165  
 Ser Ser Val Arg Leu Lys Cys Val Ala Ser Gly His Pro Arg Pro  
 170 175 180  
 Asp Ile Thr Trp Met Lys Asp Asp Gln Ala Leu Thr Arg Pro Glu  
 185 190 195  
 Ala Ala Glu Pro Arg Lys Lys Lys Trp Thr Leu Ser Leu Lys Asn  
 200 205 210  
 Leu Arg Pro Glu Asp Ser Gly Lys Tyr Thr Cys Arg Val Ser Asn  
 215 220 225  
 Arg Ala Gly Ala Ile Asn Ala Thr Tyr Lys Val Asp Val Ile Gln  
 230 235 240

Arg	Thr	Arg	Ser	Lys	Pro	Val	Leu	Thr	Gly	Thr	His	Pro	Val	Asn	
				245					250					255	
Thr	Thr	Val	Asp	Phe	Gly	Gly	Thr	Thr	Ser	Phe	Gln	Cys	Lys	Val	
				260					265					270	
Arg	Ser	Asp	Val	Lys	Pro	Val	Ile	Gln	Trp	Leu	Lys	Arg	Val	Glu	
				275					280					285	
Tyr	Gly	Ala	Glu	Gly	Arg	His	Asn	Ser	Thr	Ile	Asp	Val	Gly	Gly	
				290					295					300	
Gln	Lys	Phe	Val	Val	Leu	Pro	Thr	Gly	Asp	Val	Trp	Ser	Arg	Pro	
				305					310					315	
Asp	Gly	Ser	Tyr	Leu	Asn	Lys	Leu	Leu	Ile	Thr	Arg	Ala	Arg	Gln	
				320					325					330	
Asp	Asp	Ala	Gly	Met	Tyr	Ile	Cys	Leu	Gly	Ala	Asn	Thr	Met	Gly	
				335					340					345	
Tyr	Ser	Phe	Arg	Ser	Ala	Phe	Leu	Thr	Val	Leu	Pro	Asp	Pro	Lys	
				350					355					360	
Pro	Pro	Gly	Pro	Pro	Val	Ala	Ser	Ser	Ser	Ser	Ala	Thr	Ser	Leu	
				365					370					375	
Pro	Trp	Pro	Val	Val	Ile	Gly	Ile	Pro	Ala	Gly	Ala	Val	Phe	Ile	
				380					385					390	
Leu	Gly	Thr	Leu	Leu	Leu	Trp	Leu	Cys	Gln	Ala	Gln	Lys	Lys	Pro	
				395					400					405	
Cys	Thr	Pro	Ala	Pro	Ala	Pro	Pro	Leu	Pro	Gly	His	Arg	Pro	Pro	
				410					415					420	
Gly	Thr	Ala	Arg	Asp	Arg	Ser	Gly	Asp	Lys	Asp	Leu	Pro	Ser	Leu	
				425					430					435	
Ala	Ala	Leu	Ser	Ala	Gly	Pro	Gly	Val	Gly	Leu	Cys	Glu	Glu	His	
				440					445					450	
Gly	Ser	Pro	Ala	Ala	Pro	Gln	His	Leu	Leu	Gly	Pro	Gly	Pro	Val	
				455					460					465	
Ala	Gly	Pro	Lys	Leu	Tyr	Pro	Lys	Leu	Tyr	Thr	Asp	Ile	His	Thr	
				470					475					480	
His	Thr	His	Thr	His	Ser	His	Thr	His	Ser	His	Val	Glu	Gly	Lys	
				485					490					495	
Val	His	Gln	His	Ile	His	Tyr	Gln	Cys							
				500											

<210> 120

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 120

cgagatgacg ccgagccccc 20

<210> 121

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 121

cggttcgaca cgcggcaggt g 21

<210> 122

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 122

tgctgctcct gctgccgccg ctgctgctgg gggccttccc gccgg 45

<210> 123

<211> 4420

<212> DNA

<213> Homo sapiens

<400> 123

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gcctgggtgt tctccttctt ggtcctggaa gtcacatctg tgttggggag 200

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accccagcat ctttgccaag cctgccgaca ccctggagag ccctggtgag 300

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 tactctgtat ttcgaaaaaa 4420

<210> 124  
 <211> 1184  
 <212> PRT  
 <213> Homo sapiens

<400> 124  
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 Val Thr Ser Val Leu Gly Arg Gln Thr Met Leu Thr Gln Ser Val  
 20 25 30  
 Arg Arg Val Gln Pro Gly Lys Lys Asn Pro Ser Ile Phe Ala Lys  
 35 40 45  
 Pro Ala Asp Thr Leu Glu Ser Pro Gly Glu Trp Thr Thr Trp Phe  
 50 55 60  
 Asn Ile Asp Tyr Pro Gly Gly Lys Gly Asp Tyr Glu Arg Leu Asp  
 65 70 75  
 Ala Ile Arg Phe Tyr Tyr Gly Asp Arg Val Cys Ala Arg Pro Leu  
 80 85 90  
 Arg Leu Glu Ala Arg Thr Thr Asp Trp Thr Pro Ala Gly Ser Thr  
 95 100 105  
 Gly Gln Val Val His Gly Ser Pro Arg Glu Gly Phe Trp Cys Leu  
 110 115 120  
 Asn Arg Glu Gln Arg Pro Gly Gln Asn Cys Ser Asn Tyr Thr Val  
 125 130 135  
 Arg Phe Leu Cys Pro Pro Gly Ser Leu Arg Arg Asp Thr Glu Arg  
 140 145 150  
 Ile Trp Ser Pro Trp Ser Pro Trp Ser Lys Cys Ser Ala Ala Cys  
 155 160 165  
 Gly Gln Thr Gly Val Gln Thr Arg Thr Arg Ile Cys Leu Ala Glu  
 170 175 180  
 Met Val Ser Leu Cys Ser Glu Ala Ser Glu Glu Gly Gln His Cys  
 185 190 195  
 Met Gly Gln Asp Cys Thr Ala Cys Asp Leu Thr Cys Pro Met Gly  
 200 205 210

Gln	Val	Asn	Ala	Asp	Cys	Asp	Ala	Cys	Met	Cys	Gln	Asp	Phe	Met	215	220	225
Leu	His	Gly	Ala	Val	Ser	Leu	Pro	Gly	Gly	Ala	Pro	Ala	Ser	Gly	230	235	240
Ala	Ala	Ile	Tyr	Leu	Leu	Thr	Lys	Thr	Pro	Lys	Leu	Leu	Thr	Gln	245	250	255
Thr	Asp	Ser	Asp	Gly	Arg	Phe	Arg	Ile	Pro	Gly	Leu	Cys	Pro	Asp	260	265	270
Gly	Lys	Ser	Ile	Leu	Lys	Ile	Thr	Lys	Val	Lys	Phe	Ala	Pro	Ile	275	280	285
Val	Leu	Thr	Met	Pro	Lys	Thr	Ser	Leu	Lys	Ala	Ala	Thr	Ile	Lys	290	295	300
Ala	Glu	Phe	Val	Arg	Ala	Glu	Thr	Pro	Tyr	Met	Val	Met	Asn	Pro	305	310	315
Glu	Thr	Lys	Ala	Arg	Arg	Ala	Gly	Gln	Ser	Val	Ser	Leu	Cys	Cys	320	325	330
Lys	Ala	Thr	Gly	Lys	Pro	Arg	Pro	Asp	Lys	Tyr	Phe	Trp	Tyr	His	335	340	345
Asn	Asp	Thr	Leu	Leu	Asp	Pro	Ser	Leu	Tyr	Lys	His	Glu	Ser	Lys	350	355	360
Leu	Val	Leu	Arg	Lys	Leu	Gln	Gln	His	Gln	Ala	Gly	Glu	Tyr	Phe	365	370	375
Cys	Lys	Ala	Gln	Ser	Asp	Ala	Gly	Ala	Val	Lys	Ser	Lys	Val	Ala	380	385	390
Gln	Leu	Ile	Val	Thr	Ala	Ser	Asp	Glu	Thr	Pro	Cys	Asn	Pro	Val	395	400	405
Pro	Glu	Ser	Tyr	Leu	Ile	Arg	Leu	Pro	His	Asp	Cys	Phe	Gln	Asn	410	415	420
Ala	Thr	Asn	Ser	Phe	Tyr	Tyr	Asp	Val	Gly	Arg	Cys	Pro	Val	Lys	425	430	435
Thr	Cys	Ala	Gly	Gln	Gln	Asp	Asn	Gly	Ile	Arg	Cys	Arg	Asp	Ala	440	445	450
Val	Gln	Asn	Cys	Cys	Gly	Ile	Ser	Lys	Thr	Glu	Glu	Arg	Glu	Ile	455	460	465
Gln	Cys	Ser	Gly	Tyr	Thr	Leu	Pro	Thr	Lys	Val	Ala	Lys	Glu	Cys	470	475	480
Ser	Cys	Gln	Arg	Cys	Thr	Glu	Thr	Arg	Ser	Ile	Val	Arg	Gly	Arg	485	490	495
Val	Ser	Ala	Ala	Asp	Asn	Gly	Glu	Pro	Met	Arg	Phe	Gly	His	Val	500	505	510
Tyr	Met	Gly	Asn	Ser	Arg	Val	Ser	Met	Thr	Gly	Tyr	Lys	Gly	Thr	515	520	525

Phe Thr Leu His	Val Pro Gln Asp Thr	Glu Arg Leu Val Leu Thr	530	535	540
Phe Val Asp Arg	Leu Gln Lys Phe Val	Asn Thr Thr Lys Val Leu	545	550	555
Pro Phe Asn Lys	Lys Gly Ser Ala Val	Phe His Glu Ile Lys Met	560	565	570
Leu Arg Arg Lys	Glu Pro Ile Thr Leu	Glu Ala Met Glu Thr Asn	575	580	585
Ile Ile Pro Leu	Gly Glu Val Val Gly	Glu Asp Pro Met Ala Glu	590	595	600
Leu Glu Ile Pro	Ser Arg Ser Phe Tyr	Arg Gln Asn Gly Glu Pro	605	610	615
Tyr Ile Gly Lys	Val Lys Ala Ser Val	Thr Phe Leu Asp Pro Arg	620	625	630
Asn Ile Ser Thr	Ala Thr Ala Ala Gln	Thr Asp Leu Asn Phe Ile	635	640	645
Asn Asp Glu Gly	Asp Thr Phe Pro Leu	Arg Thr Tyr Gly Met Phe	650	655	660
Ser Val Asp Phe	Arg Asp Glu Val Thr	Ser Glu Pro Leu Asn Ala	665	670	675
Gly Lys Val Lys	Val His Leu Asp Ser	Thr Gln Val Lys Met Pro	680	685	690
Glu His Ile Ser	Thr Val Lys Leu Trp	Ser Leu Asn Pro Asp Thr	695	700	705
Gly Leu Trp Glu	Glu Glu Gly Asp Phe	Lys Phe Glu Asn Gln Arg	710	715	720
Arg Asn Lys Arg	Glu Asp Arg Thr Phe	Leu Val Gly Asn Leu Glu	725	730	735
Ile Arg Glu Arg	Arg Leu Phe Asn Leu	Asp Val Pro Glu Ser Arg	740	745	750
Arg Cys Phe Val	Lys Val Arg Ala Tyr	Arg Ser Glu Arg Phe Leu	755	760	765
Pro Ser Glu Gln	Ile Gln Gly Val Val	Ile Ser Val Ile Asn Leu	770	775	780
Glu Pro Arg Thr	Gly Phe Leu Ser Asn	Pro Arg Ala Trp Gly Arg	785	790	795
Phe Asp Ser Val	Ile Thr Gly Pro Asn	Gly Ala Cys Val Pro Ala	800	805	810
Phe Cys Asp Asp	Gln Ser Pro Asp Ala	Tyr Ser Ala Tyr Val Leu	815	820	825
Ala Ser Leu Ala	Gly Glu Glu Leu Gln	Ala Val Glu Ser Ser Pro	830	835	840

Lys	Phe	Asn	Pro	Asn	Ala	Ile	Gly	Val	Pro	Gln	Pro	Tyr	Leu	Asn		845	850	855
Lys	Leu	Asn	Tyr	Arg	Arg	Thr	Asp	His	Glu	Asp	Pro	Arg	Val	Lys		860	865	870
Lys	Thr	Ala	Phe	Gln	Ile	Ser	Met	Ala	Lys	Pro	Arg	Pro	Asn	Ser		875	880	885
Ala	Glu	Glu	Ser	Asn	Gly	Pro	Ile	Tyr	Ala	Phe	Glu	Asn	Leu	Arg		890	895	900
Ala	Cys	Glu	Glu	Ala	Pro	Pro	Ser	Ala	Ala	His	Phe	Arg	Phe	Tyr		905	910	915
Gln	Ile	Glu	Gly	Asp	Arg	Tyr	Asp	Tyr	Asn	Thr	Val	Pro	Phe	Asn		920	925	930
Glu	Asp	Asp	Pro	Met	Ser	Trp	Thr	Glu	Asp	Tyr	Leu	Ala	Trp	Trp		935	940	945
Pro	Lys	Pro	Met	Glu	Phe	Arg	Ala	Cys	Tyr	Ile	Lys	Val	Lys	Ile		950	955	960
Val	Gly	Pro	Leu	Glu	Val	Asn	Val	Arg	Ser	Arg	Asn	Met	Gly	Gly		965	970	975
Thr	His	Arg	Arg	Thr	Val	Gly	Lys	Leu	Tyr	Gly	Ile	Arg	Asp	Val		980	985	990
Arg	Ser	Thr	Arg	Asp	Arg	Asp	Gln	Pro	Asn	Val	Ser	Ala	Ala	Cys		995	1000	1005
Leu	Glu	Phe	Lys	Cys	Ser	Gly	Met	Leu	Tyr	Asp	Gln	Asp	Arg	Val		1010	1015	1020
Asp	Arg	Thr	Leu	Val	Lys	Val	Ile	Pro	Gln	Gly	Ser	Cys	Arg	Arg		1025	1030	1035
Ala	Ser	Val	Asn	Pro	Met	Leu	His	Glu	Tyr	Leu	Val	Asn	His	Leu		1040	1045	1050
Pro	Leu	Ala	Val	Asn	Asn	Asp	Thr	Ser	Glu	Tyr	Thr	Met	Leu	Ala		1055	1060	1065
Pro	Leu	Asp	Pro	Leu	Gly	His	Asn	Tyr	Gly	Ile	Tyr	Thr	Val	Thr		1070	1075	1080
Asp	Gln	Asp	Pro	Arg	Thr	Ala	Lys	Glu	Ile	Ala	Leu	Gly	Arg	Cys		1085	1090	1095
Phe	Asp	Gly	Thr	Ser	Asp	Gly	Ser	Ser	Arg	Ile	Met	Lys	Ser	Asn		1100	1105	1110
Val	Gly	Val	Ala	Leu	Thr	Phe	Asn	Cys	Val	Glu	Arg	Gln	Val	Gly		1115	1120	1125
Arg	Gln	Ser	Ala	Phe	Gln	Tyr	Leu	Gln	Ser	Thr	Pro	Ala	Gln	Ser		1130	1135	1140
Pro	Ala	Ala	Gly	Thr	Val	Gln	Gly	Arg	Val	Pro	Ser	Arg	Arg	Gln		1145	1150	1155

Gln Arg Ala Ser Arg Gly Gly Gln Arg Gln Gly Gly Val Val Ala  
 1160 1165 1170

Ser Leu Arg Phe Pro Arg Val Ala Gln Gln Pro Leu Ile Asn  
 1175 1180

<210> 125  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 125  
 ctggtgcctc aacagggagc ag 22

<210> 126  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 126  
 ccattgtgca ggtcaggtca cag 23

<210> 127  
 <211> 40  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 127  
 ctggagcaag tgctcagctg cctgtggtca gactgggggtc 40

<210> 128  
 <211> 2819  
 <212> DNA  
 <213> Homo sapiens

<400> 128  
 ctgcaagttg ttaacgccta acacacaagt atgttaggct tccaccaaag 50  
 tcctcaatat acctgaatac gcacaatatc ttaactcttc atatttggtt 100  
 ttgggatctg ctttgaggtc ccatcttcat ttaaaaaaaaa atacagagac 150  
 ctacctaccc gtacgcatac atacatatgt gtatatatat gtaaaactaga 200  
 caaagatcgc agatcataaa gcaagctctg ctttagtttc caagaagatt 250  
 acaaagaatt tagagatgta tttgtcaaga tccctgtcga ttcatgccct 300  
 ttgggttacg gtgtcctcag tgatgcagcc ctaccctttg gtttggggac 350  
 attatgattt gtgtaagact cagatttaca cggaagaagg gaaagtttgg 400  
 gattacatgg cctgccagcc ggaatccacg gacatgacaa aatatctgaa 450

agtgaaactc gatcctccgg atattacctg tggagaccct cctgagacgt 500  
 tctgtgcaat gggcaatccc tacatgtgca ataatgagtg tgatgcgagt 550  
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 ctctccaggt taacatcact ctgtcttgga gcaaaacat tgagctaaca 700  
 gacaacatag ttattacctt tgaatctggg cgtccagacc aaatgatcct 750  
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 ccacagactg cttagatgct ttccacatgg atcctaaatc cgtgaaggat 850  
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 agggatataca acaaatagca aaataatcca ctttgaaatc aaagacaggt 950  
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 cagctggata caaccaagaa actcagagat ttctttacag tcacagacct 1050  
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 atccccaag gcaactgcaa tacctgtatc occagtattt ccagtattgg 1350  
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 gccacaacaa cgtgcgctgc ctgtgcccg cgcatacac gggcatcctc 1450  
 tgcgagaagc tgcggtgca ggaggctggc agctgcggtc ccgactctgg 1500  
 ccagggcgcg ccccgcacg gcaccccgag gctgctgctg ctgaccacgc 1550  
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ccctcgttgg ttgaaagatt tctttgtctg atgttagtga tgcacatgtg 2150  
taacagcccc ctctaaaagc gcaagccagt catacccctg tatatcttag 2200  
cagcactgag tccagtgcga gcacacaccc actatacaag agtggctata 2250  
ggaaaaaaga aagtgtatct atccttttgt attcaaataga agttattttt 2300  
cttgaactac tgtaatatgt agattttttg tattattgcc aatttgtgtt 2350  
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gctttaacac tggaagattt aaagaataaa aactcctgca taaacgattt 2600  
caggaatttg tattgcaatt tottaagatg aaaggaacag ccaccaagca 2650  
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acgaatttag ttcccaggaa gatggattga tgttcactag cttggacaac 2750  
ttctgcaaaa tatgagacta tttccacttg ggaaaaatta caacagcaaa 2800  
aaaaaaaaa aaaaaaaaaa 2819

<210> 129

<211> 438

<212> PRT

<213> Homo sapiens

<400> 129

Met	Tyr	Leu	Ser	Arg	Ser	Leu	Ser	Ile	His	Ala	Leu	Trp	Val	Thr
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Val	Ser	Ser	Val	Met	Gln	Pro	Tyr	Pro	Leu	Val	Trp	Gly	His	Tyr
				20					25					30
Asp	Leu	Cys	Lys	Thr	Gln	Ile	Tyr	Thr	Glu	Glu	Gly	Lys	Val	Trp
				35					40					45
Asp	Tyr	Met	Ala	Cys	Gln	Pro	Glu	Ser	Thr	Asp	Met	Thr	Lys	Tyr
				50					55					60
Leu	Lys	Val	Lys	Leu	Asp	Pro	Pro	Asp	Ile	Thr	Cys	Gly	Asp	Pro
				65					70					75
Pro	Glu	Thr	Phe	Cys	Ala	Met	Gly	Asn	Pro	Tyr	Met	Cys	Asn	Asn
				80					85					90
Glu	Cys	Asp	Ala	Ser	Thr	Pro	Glu	Leu	Ala	His	Pro	Pro	Glu	Leu
				95					100					105
Met	Phe	Asp	Phe	Glu	Gly	Arg	His	Pro	Ser	Thr	Phe	Trp	Gln	Ser
				110					115					120
Ala	Thr	Trp	Lys	Glu	Tyr	Pro	Lys	Pro	Leu	Gln	Val	Asn	Ile	Thr



[illegible]

<210> 130  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 130  
tcgattatgg acgaacatgg cagc 24

<210> 131  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 131  
ttctgagatc cctcatcctc 20

<210> 132  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 132  
aggttcaggg acagcaagtt tggg 24

<210> 133  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 133  
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<210> 134  
<211> 1493  
<212> DNA  
<213> Homo sapiens

<400> 134  
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ccgggcgagg tgtcctcatg acttctcttg tggaccatgt ccgtgatctt 150  
ttttgcctgc gtggtacggg taagggatgg actgccctc tcagcctcta 200  
ctgattttta ccacacccaa gatttttttg aatggaggag acggctcaag 250  
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ctatctgctc ctgccagtgt ccagcagcca tggccttctg cttcctggag 400  
accctgtggt gggaattcac agcttcctat gacactacct gcattggcct 450  
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acttgagacc tgctcctaatt ttccgaatgg aaccagtgc acgcctgggt 700  
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gctggttgga ccaaacctcg tgagccagcc acccctgacc caaatgagga 850  
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gggaaatctc atcagcaggg agcctgtgga aaagggcatg tcagtgaat 950  
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gctgttgccc acaagcgcct tttatttagg gtaaaattaa caaatccatt 1050  
ctattcctct gacctatgct tagtacatat gacctttaac ccttacattt 1100  
atatgattct ggggttgctt cagaagtgtt atttcatgaa tcattcatat 1150  
gatttgatcc ccaggattc tattttgttt aatgggcttt tctactaaaa 1200  
gcataaaata ctgaggctga tttagtcagg gcaaaaccat ttactttaca 1250  
tattcgtttt caatacttgc tgttcatgtt acacaagctt cttacggttt 1300  
tcttgtaaca ataaatattt tgagtaaata atgggtacat tttaacaaac 1350  
tcagtagtac aacctaaact tgtataaaag tgtgtaaaaa tgtatagcca 1400  
tttatatcct atgtataaat taaatgaggt ggcttcagaa atggcagaat 1450  
aaatctaaag tgttttattaa aaaaaaaaaa aaaaaaaaaa aag 1493

<210> 135

<211> 228

<212> PRT

<213> Homo sapiens

<400> 135

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Leu	Pro	Leu	Ser	Ala	Ser	Thr	Asp	Phe	Tyr	His	Thr	Gln	Asp	Phe
				20				25						30

Leu	Glu	Trp	Arg	Arg	Arg	Leu	Lys	Ser	Leu	Ala	Leu	Arg	Leu	Ala
				35				40						45

Gln	Tyr	Pro	Gly	Arg	Gly	Ser	Ala	Glu	Gly	Cys	Asp	Phe	Ser	Ile	
				50					55					60	
His	Phe	Ser	Ser	Phe	Gly	Asp	Val	Ala	Cys	Met	Ala	Ile	Cys	Ser	
				65					70					75	
Cys	Gln	Cys	Pro	Ala	Ala	Met	Ala	Phe	Cys	Phe	Leu	Glu	Thr	Leu	
				80					85					90	
Trp	Trp	Glu	Phe	Thr	Ala	Ser	Tyr	Asp	Thr	Thr	Cys	Ile	Gly	Leu	
				95					100					105	
Ala	Ser	Arg	Pro	Tyr	Ala	Phe	Leu	Glu	Phe	Asp	Ser	Ile	Ile	Gln	
				110					115					120	
Lys	Val	Lys	Trp	His	Phe	Asn	Tyr	Val	Ser	Ser	Ser	Gln	Met	Glu	
				125					130					135	
Cys	Ser	Leu	Glu	Lys	Ile	Gln	Glu	Glu	Leu	Lys	Leu	Gln	Pro	Pro	
				140					145					150	
Ala	Val	Leu	Thr	Leu	Glu	Asp	Thr	Asp	Val	Ala	Asn	Gly	Val	Met	
				155					160					165	
Asn	Gly	His	Thr	Pro	Met	His	Leu	Glu	Pro	Ala	Pro	Asn	Phe	Arg	
				170					175					180	
Met	Glu	Pro	Val	Thr	Ala	Leu	Gly	Ile	Leu	Ser	Leu	Ile	Leu	Asn	
				185					190					195	
Ile	Met	Cys	Ala	Ala	Leu	Asn	Leu	Ile	Arg	Gly	Val	His	Leu	Ala	
				200					205					210	
Glu	His	Ser	Leu	Gln	Asp	Pro	Arg	Ser	Trp	Phe	Cys	Trp	Leu	Asp	
				215					220					225	
Gln	Thr	Ser													

<210> 136  
 <211> 239  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 39, 61, 143, 209  
 <223> unknown base

<400> 136  
 tgcttcctgg agaccctgtg gtgggaattc acagcttcnt atgacactac 50  
 ctgcattggc ntagcctcca ggccatacgc ttttcttgag tttgacagca 100  
 tcattcagaa agtgaagtgg cattttaact atgtaagttc cnttcagatg 150  
 gagtgcagct tggaaaaaat tcaggaggag ctcaagttgc agcctccagc 200  
 ggtttcant atggaggaca cagatgtggc aaatgggggt 239

<210> 137  
 <211> 2300  
 <212> DNA

[illegible]

<400> 137

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ccctttaaaa	cgaggcgggt	ggtgcctgcc	cctttaaggg	cggggcgtcc	150
ggacgactgt	atctgagccc	cagactgccc	cgagtttctg	tgcaggctg	200
cgaggaaagg	cccctaggct	gggtctgggt	gcttggcggc	ggcggtctcc	250
tccccgctcg	tctccccgg	gcccagaggc	acctcggtt	cagtcatgct	300
gagcagagta	tggaagcacc	tgactacgaa	gtgctatccg	tgcgagaaca	350
gctattccac	gagaggatcc	gcgagtgtat	tatatcaaca	cttctgtttg	400
caacactgta	catcctctgc	cacatcttcc	tgaccgcgtt	caagaagcct	450
gctgagttca	ccacagtgga	tgatgaagat	gccaccgtca	acaagattgc	500
gctcgagctg	tgcaccttta	ccctggcaat	tgccctgggt	gctgtcctgc	550
tcctgccctt	ctccatcctc	agcaatgagg	tgctgctctc	cctgcctcgg	600
aactactaca	tccagtggct	caacggctcc	ctcatccatg	gcctctggaa	650
ccttgttttt	ctcttcccca	acctgtccct	catcttctct	atgccctttg	700
catatttctt	cactgagtct	gagggccttg	ctggctccag	aaagggtgtc	750
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ccaacagaga	gtcactctat	gacttttggg	agtactatct	cccctacctc	900
tactcatgca	tctccttct	tggggttctg	ctgctcctgg	tgtgtactcc	950
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ccgggctgct	ggaagacctg	gaggagcagc	tgtactgctc	agcctttgag	1050
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<210> 138

<211> 489

<212> PRT

<213> Homo sapiens

<400> 138

Met	Glu	Ala	Pro	Asp	Tyr	Glu	Val	Leu	Ser	Val	Arg	Glu	Gln	Leu
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Phe	His	Glu	Arg	Ile	Arg	Glu	Cys	Ile	Ile	Ser	Thr	Leu	Leu	Phe
				20					25					30
Ala	Thr	Leu	Tyr	Ile	Leu	Cys	His	Ile	Phe	Leu	Thr	Arg	Phe	Lys
				35					40					45
Lys	Pro	Ala	Glu	Phe	Thr	Thr	Val	Asp	Asp	Glu	Asp	Ala	Thr	Val
				50					55					60
Asn	Lys	Ile	Ala	Leu	Glu	Leu	Cys	Thr	Phe	Thr	Leu	Ala	Ile	Ala
				65					70					75
Leu	Gly	Ala	Val	Leu	Leu	Leu	Pro	Phe	Ser	Ile	Ile	Ser	Asn	Glu
				80					85					90
Val	Leu	Leu	Ser	Leu	Pro	Arg	Asn	Tyr	Tyr	Ile	Gln	Trp	Leu	Asn
				95					100					105
Gly	Ser	Leu	Ile	His	Gly	Leu	Trp	Asn	Leu	Val	Phe	Leu	Phe	Pro
				110					115					120
Asn	Leu	Ser	Leu	Ile	Phe	Leu	Met	Pro	Phe	Ala	Tyr	Phe	Phe	Thr

				125					130				135	
Glu	Ser	Glu	Gly	Phe	Ala	Gly	Ser	Arg	Lys	Gly	Val	Leu	Gly	Arg
				140					145					150
Val	Tyr	Glu	Thr	Val	Val	Met	Leu	Met	Leu	Leu	Thr	Leu	Leu	Val
				155					160					165
Leu	Gly	Met	Val	Trp	Val	Ala	Ser	Ala	Ile	Val	Asp	Lys	Asn	Lys
				170					175					180
Ala	Asn	Arg	Glu	Ser	Leu	Tyr	Asp	Phe	Trp	Glu	Tyr	Tyr	Leu	Pro
				185					190					195
Tyr	Leu	Tyr	Ser	Cys	Ile	Ser	Phe	Leu	Gly	Val	Leu	Leu	Leu	Leu
				200					205					210
Val	Cys	Thr	Pro	Leu	Gly	Leu	Ala	Arg	Met	Phe	Ser	Val	Thr	Gly
				215					220					225
Lys	Leu	Leu	Val	Lys	Pro	Arg	Leu	Leu	Glu	Asp	Leu	Glu	Glu	Gln
				230					235					240
Leu	Tyr	Cys	Ser	Ala	Phe	Glu	Glu	Ala	Ala	Leu	Thr	Arg	Arg	Ile
				245					250					255
Cys	Asn	Pro	Thr	Ser	Cys	Trp	Leu	Pro	Leu	Asp	Met	Glu	Leu	Leu
				260					265					270
His	Arg	Gln	Val	Leu	Ala	Leu	Gln	Thr	Gln	Arg	Val	Leu	Leu	Glu
				275					280					285
Lys	Arg	Arg	Lys	Ala	Ser	Ala	Trp	Gln	Arg	Asn	Leu	Gly	Tyr	Pro
				290					295					300
Leu	Ala	Met	Leu	Cys	Leu	Leu	Val	Leu	Thr	Gly	Leu	Ser	Val	Leu
				305					310					315
Ile	Val	Ala	Ile	His	Ile	Leu	Glu	Leu	Leu	Ile	Asp	Glu	Ala	Ala
				320					325					330
Met	Pro	Arg	Gly	Met	Gln	Gly	Thr	Ser	Leu	Gly	Gln	Val	Ser	Phe
				335					340					345
Ser	Lys	Leu	Gly	Ser	Phe	Gly	Ala	Val	Ile	Gln	Val	Val	Leu	Ile
				350					355					360
Phe	Tyr	Leu	Met	Val	Ser	Ser	Val	Val	Gly	Phe	Tyr	Ser	Ser	Pro
				365					370					375
Leu	Phe	Arg	Ser	Leu	Arg	Pro	Arg	Trp	His	Asp	Thr	Ala	Met	Thr
				380					385					390
Gln	Ile	Ile	Gly	Asn	Cys	Val	Cys	Leu	Leu	Val	Leu	Ser	Ser	Ala
				395					400					405
Leu	Pro	Val	Phe	Ser	Arg	Thr	Leu	Gly	Leu	Thr	Arg	Phe	Asp	Leu
				410					415					420
Leu	Gly	Asp	Phe	Gly	Arg	Phe	Asn	Trp	Leu	Gly	Asn	Phe	Tyr	Ile
				425					430					435
Val	Phe	Leu	Tyr	Asn	Ala	Ala	Phe	Ala	Gly	Leu	Thr	Thr	Leu	Cys

	440		445		450
Leu Val Lys Thr Phe Thr Ala Ala Val Arg Ala Glu Leu Ile Arg					
	455		460		465
Ala Phe Gly Leu Asp Arg Leu Pro Leu Pro Val Ser Gly Phe Pro					
	470		475		480
Gln Ala Ser Arg Lys Thr Gln His Gln					
	485				

<210> 139  
 <211> 294  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 53, 57  
 <223> unknown base

<400> 139  
 ggctgccgag ggaaggcccc ttgggttggt cttggttgct tggcggcggc 50  
 ggnttcntcc ccgctcgtcc tccccgggcc cagaggcacc tcggcttcag 100  
 tcatgctgag cagagtatgg aagcacctga ctacgaagtg ctatccgtgc 150  
 gagaacagct attccacgag aggatccgcg agtgtattat atcaaacatt 200  
 ctgtttgcaa cactgtacat cctctgccac atcttctga cccgcttcaa 250  
 gaagcctgct gaggtcacca cagtggatga tgaagatgcc accg 294

<210> 140  
 <211> 526  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 197, 349  
 <223> unknown base

<400> 140  
 gaccgacctt aaagagtggg agcaaaggga ggacagagcc ttttaaaacg 50  
 aggcgggtggg gcctgccctt taagggcggg gcgtccggac gactgtatct 100  
 gagccccaga ctgccccgag tttctgtcgc aggctgcgag gaaaggcccc 150  
 taggctgggt ctggtgcttg gcggcgggcg cttcctcccc gttgtcntcc 200  
 ccggggcccag aggcacctcg gcttcagtca tgctgagcag agtatggaag 250  
 cacctgacta cgaagtgcta tccgtgcgag aacagctatt ccacgagagg 300  
 atccgcgagt gtattatatt aacactttctg tttgcaaacac tgtacatcnt 350  
 ctgccacatc ttctgacctt gcttcaagaa gcctgctgag ttaccacag 400  
 tggatgatga agatgccacc gtcaacaaga ttgcgctcga gctgtgcacc 450



tttaccctgg caattgccct ggggtgctgtc ctgctcctgc ctttctccat 500

catcagcaat gaggtgctgc actccc 526

<210> 141

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 141

gactgtatct gagccccaga ctgc 24

<210> 142

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 142

tcagcaatga ggtgctgtc 20

<210> 143

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 143

tgaggaagat gagggacagg ttgg 24

<210> 144

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 144

tatggaagca cctgactacg aagtgtatc cgtgcgagaa cagctattcc 50

<210> 145

<211> 685

<212> DNA

<213> Homo sapiens

<400> 145

gatgtgctcc ttggagctgg tgtgcagtgt cctgactgta agatcaagtc 50

caaacctgtt ttggaattga ggaaacttct cttttgatct cagcccttgg 100

tgggtccaggt cttcatgctg ctgtgggtga tattactggc cctggctcct 150

gtcagtggtgac agtttgcaag gacacccagg cccattattt tcctccagcc 200

tccatggacc acagtcttcc aaggagagag agtgaccctc acttgcaagg 250

gatttcgctt ctactcacca cagaaaacaa aatggtacca tcggtacctt 300  
 gggaaagaaa tactaagaga aaccccagac aatataccttg aggttcagga 350  
 atctggagag tacagatgcc aggcccaggg ctcccctctc agtagccctg 400  
 tgcacttgga tttttcttca gagatgggat ttctctcatgc tgcccaggct 450  
 aatgttgaac tcctgggctc aagtgatctg ctcacctagg cctctcaaag 500  
 cgctgggatt acagcttcgc tgatcctgca agctccactt tctgtgtttg 550  
 aaggagactc tgtggttctg aggtgccggg caaaggcgga agtaacactg 600  
 aataatacta tttacaagaa tgataatgtc ctggcattcc ttaataaaaag 650  
 aactgacttc caaaaaaaaa aaaaaaaaaa aaaaa 685

<210> 146  
 <211> 124  
 <212> PRT  
 <213> Homo sapiens

<400> 146  
 Met Leu Leu Trp Val Ile Leu Leu Val Leu Ala Pro Val Ser Gly  
 1 5 10 15  
 Gln Phe Ala Arg Thr Pro Arg Pro Ile Ile Phe Leu Gln Pro Pro  
 20 25 30  
 Trp Thr Thr Val Phe Gln Gly Glu Arg Val Thr Leu Thr Cys Lys  
 35 40 45  
 Gly Phe Arg Phe Tyr Ser Pro Gln Lys Thr Lys Trp Tyr His Arg  
 50 55 60  
 Tyr Leu Gly Lys Glu Ile Leu Arg Glu Thr Pro Asp Asn Ile Leu  
 65 70 75  
 Glu Val Gln Glu Ser Gly Glu Tyr Arg Cys Gln Ala Gln Gly Ser  
 80 85 90  
 Pro Leu Ser Ser Pro Val His Leu Asp Phe Ser Ser Glu Met Gly  
 95 100 105  
 Phe Pro His Ala Ala Gln Ala Asn Val Glu Leu Leu Gly Ser Ser  
 110 115 120  
 Asp Leu Leu Thr

<210> 147  
 <211> 1621  
 <212> DNA  
 <213> Homo sapiens

<400> 147  
 cagaagaggg ggctagctag ctgtctctgc ggaccaggga gacccccgcg 50  
 cccccccggt gtgaggcggc ctcacagggc cgggtgggct ggcgagccga 100  
 cgcggcggcg gaggaggctg tgaggagtgt gtggaacagg acccgggaca 150

gaggaaccat ggctccgcag aacctgagca ctttttgcct gttgctgcta 200  
 tacctcatcg gggcgggtgat tgccggacga gatttctata agatcttggg 250  
 ggtgcctcga agtgccctcta taaaggatat taaaaaggcc tataggaaac 300  
 tagccctgca gcttcatccc gaccggaacc ctgatgatcc acaagcccag 350  
 gagaaattcc aggatctggg tgctgcttat gaggttctgt cagatagtga 400  
 gaaacggaaa cagtacgata cttatggtga agaaggatta aaagatggtc 450  
 atcagagctc ccatggagac attttttcac acttctttgg ggattttggt 500  
 ttcatgtttg gaggaacccc tcgtcagcaa gacagaaata ttccaagagg 550  
 aagtgatatt attgtagatc tagaagtcac tttggaagaa gtatatgcag 600  
 gaaattttgt ggaagtagtt agaaacaaac ctgtggcaag gcaggctcct 650  
 ggcaaacgga agtgcaattg tcggcaagag atgcggacca ccagctggg 700  
 ccctgggcgc ttccaaatga ccaggagggt ggtctgcgac gaatgcccta 750  
 atgtcaaact agtgaatgaa gaacgaacgc tggaagtaga aatagagcct 800  
 ggggtgagag acggcatgga gtaccctttt attggagaag gtgagcctca 850  
 cgtggatggg gagcctggag atttacggtt ccgaatcaaa gttgtcaagc 900  
 acccaatatt tgaaaggaga ggagatgatt tgtacacaaa tgtgacaatc 950  
 tcattagtgt agtcaactggg tggctttgag atggatatta ctcaacttga 1000  
 tggtcacaag gtacatattt cccgggataa gatcaccagg ccaggagcga 1050  
 agctatggaa gaaaggggaa gggctcccca actttgacaa caacaatatc 1100  
 aagggctctt tgataatcac ttttgatgtg gattttccaa aagaacagtt 1150  
 aacagaggaa gcgagagaag gtatcaaaca gctactgaaa caagggtcag 1200  
 tgcagaaggt atacaatgga ctgcaaggat attgagagtg aataaaaattg 1250  
 gactttgttt aaaataagtg aataagcgat atttattatc tgcaagggtt 1300  
 ttttgtgtgt gtttttgttt ttattttcaa tatgcaagtt aggcttaatt 1350  
 tttttatcta atgatcatca tgaaatgaat aagagggctt aagaatttgt 1400  
 ccatttgcac tcggaaaaga atgaccagca aaaggtttac taataacctc 1450  
 ccctttgggg atttaatgtc tgggtgctgcc gcctgagttt caagaattaa 1500  
 agctgcaaga ggactccagg agcaaaagaa acacaatata gagggtttga 1550  
 gttgttagca atttcattca aaatgccaac tggagaagtc tgttttttaa 1600  
 tacattttgt tgttattttt a 1621

<210> 148  
 <211> 358  
 <212> PRT

<213> Homo sapiens

<400> 148

Met	Ala	Pro	Gln	Asn	Leu	Ser	Thr	Phe	Cys	Leu	Leu	Leu	Leu	Tyr
1				5					10					15
Leu	Ile	Gly	Ala	Val	Ile	Ala	Gly	Arg	Asp	Phe	Tyr	Lys	Ile	Leu
				20					25					30
Gly	Val	Pro	Arg	Ser	Ala	Ser	Ile	Lys	Asp	Ile	Lys	Lys	Ala	Tyr
				35					40					45
Arg	Lys	Leu	Ala	Leu	Gln	Leu	His	Pro	Asp	Arg	Asn	Pro	Asp	Asp
				50					55					60
Pro	Gln	Ala	Gln	Glu	Lys	Phe	Gln	Asp	Leu	Gly	Ala	Ala	Tyr	Glu
				65					70					75
Val	Leu	Ser	Asp	Ser	Glu	Lys	Arg	Lys	Gln	Tyr	Asp	Thr	Tyr	Gly
				80					85					90
Glu	Glu	Gly	Leu	Lys	Asp	Gly	His	Gln	Ser	Ser	His	Gly	Asp	Ile
				95					100					105
Phe	Ser	His	Phe	Phe	Gly	Asp	Phe	Gly	Phe	Met	Phe	Gly	Gly	Thr
				110					115					120
Pro	Arg	Gln	Gln	Asp	Arg	Asn	Ile	Pro	Arg	Gly	Ser	Asp	Ile	Ile
				125					130					135
Val	Asp	Leu	Glu	Val	Thr	Leu	Glu	Glu	Val	Tyr	Ala	Gly	Asn	Phe
				140					145					150
Val	Glu	Val	Val	Arg	Asn	Lys	Pro	Val	Ala	Arg	Gln	Ala	Pro	Gly
				155					160					165
Lys	Arg	Lys	Cys	Asn	Cys	Arg	Gln	Glu	Met	Arg	Thr	Thr	Gln	Leu
				170					175					180
Gly	Pro	Gly	Arg	Phe	Gln	Met	Thr	Gln	Glu	Val	Val	Cys	Asp	Glu
				185					190					195
Cys	Pro	Asn	Val	Lys	Leu	Val	Asn	Glu	Glu	Arg	Thr	Leu	Glu	Val
				200					205					210
Glu	Ile	Glu	Pro	Gly	Val	Arg	Asp	Gly	Met	Glu	Tyr	Pro	Phe	Ile
				215					220					225
Gly	Glu	Gly	Glu	Pro	His	Val	Asp	Gly	Glu	Pro	Gly	Asp	Leu	Arg
				230					235					240
Phe	Arg	Ile	Lys	Val	Val	Lys	His	Pro	Ile	Phe	Glu	Arg	Arg	Gly
				245					250					255
Asp	Asp	Leu	Tyr	Thr	Asn	Val	Thr	Ile	Ser	Leu	Val	Glu	Ser	Leu
				260					265					270
Val	Gly	Phe	Glu	Met	Asp	Ile	Thr	His	Leu	Asp	Gly	His	Lys	Val
				275					280					285
His	Ile	Ser	Arg	Asp	Lys	Ile	Thr	Arg	Pro	Gly	Ala	Lys	Leu	Trp
				290					295					300

Lys Lys Gly Glu Gly Leu Pro Asn Phe Asp Asn Asn Asn Ile Lys  
305 310 315

Gly Ser Leu Ile Ile Thr Phe Asp Val Asp Phe Pro Lys Glu Gln  
320 325 330

Leu Thr Glu Glu Ala Arg Glu Gly Ile Lys Gln Leu Leu Lys Gln  
335 340 345

Gly Ser Val Gln Lys Val Tyr Asn Gly Leu Gln Gly Tyr  
350 355

<210> 149  
<211> 509  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 34, 52, 134, 142, 155, 158, 196, 217, 228, 272, 347, 410, 445,  
482  
<223> unknown base

<400> 149  
tgggaccagg gaaccccggtg ccccccgggtg gagngcctaa caggccgggtg 50  
gntgcgaccg aagcggcggtg cggaggaggt tttgaggatt tttggaacag 100  
gacccggaca gaggaaccat ggttccgcag aacntgagca cnttttgcct 150  
gttgntgnta tacttcatcg gggcggtgat tgccggacga gatttntata 200  
agattttggg gtgcctngaa gtgccttnta taaaggatat taaaaaggcc 250  
tataggaaac tagccctgca gntttatccc gaccggaacc ctgatgatcc 300  
acaagcccag gagaaattcc aggatttggg tgctgcttat gaggttntgt 350  
cagatagtga gaaacggaaa cagtacgata attatggtga agaaggatta 400  
aaagatggtg atcagagctc ccatggagac attttttcac acttntttgg 450  
ggattttggg ttcattgttg gaggaacccc tngtcagcaa gacagaaata 500  
ttccaagag 509

<210> 150  
<211> 1532  
<212> DNA  
<213> Homo sapiens

<400> 150  
ggcacgaggc ggcggggcag tcgcgggatg cgcccgggag ccacagcctg 50  
aggccctcag gtctctgcag gtgtcgtgga ggaacctagc acctgccatc 100  
ctcttcccca atttgccact tccagcagct ttagcccatg aggaggatgt 150  
gaccgggact gagtcaggag ccctctggaa gcatggagac tgtggtgatt 200  
gttgccatag gtgtgctggc caccatcttt ctggcttcgt ttgcagcctt 250  
ggtgctggtt tgcaggcagc gctactgccg gccgcgagac ctgctgcagc 300

gctatgattc taagcccatt gtggacctca ttggtgccat ggagacccag 350  
tctgagccct ctgagttaga actggaogat gtcgttatca ccaaccccca 400  
cattgaggcc attctggaga atgaagactg gatcgaagat gcctcgggtc 450  
tcatgtccca ctgcattgcc atcttgaaga tttgtcacac tctgacagag 500  
aagcttggtg ccatgacaat gggctctggg gccaaagatga agacttcagc 550  
cagtgtcagc gacatcattg tggtggtccaa gcggtatcagc cccaggggtg 600  
atgatgttgt gaagtcgatg taccctccgt tggaccccaa actcctggac 650  
gcacggacga ctgccctgct cctgtctgtc agtcacctgg tgctgggtgac 700  
aaggaatgcc tgccatctga cgggaggcct ggactggatt gaccagtctc 750  
tgtcggctgc tgaggagcat ttggaagtcc ttcgagaagc agccctagct 800  
tctgagccag ataaaggcct cccaggccct gaaggcttcc tgcaggagca 850  
gtctgcaatt tagtgctac aggccagcag ctagccatga agggccctgc 900  
cgccatccct ggatggctca gcttagcctt ctactttttc ctatagagtt 950  
agttgttttc cacggctgga gagttcagct gtgtgtgcat agtaaagcag 1000  
gagatccccg tcagtttatg cctcttttgc agttgcaaac tgtggctggt 1050  
gagtggcagt ctaatactac agttagggga gatgccattc actctctgca 1100  
agaggagtat tgaaaactgg tggactgtca gctttattta gctcacctag 1150  
tgttttcaag aaaattgagc caccgtctaa gaaatcaaga ggtttcacat 1200  
taaaattaga atttctggcc tctctcgatc ggtcagaatg tgtggcaatt 1250  
ctgatctgca ttttcagaag aggacaatca attgaaacta agtaggggtt 1300  
tcttcttttg gcaagacttg tactctctca cctggcctgt ttcatttatt 1350  
tgtattatct gcctgggtccc tgaggcgtct gggctctctcc tctcccttgc 1400  
aggtttgggt ttgaagctga ggaactacaa agttgatgat ttctttttta 1450  
tctttatgcc tgcaatttta cctagctacc actaggtgga tagtaaattt 1500  
atacttatgt ttccctcaaa aaaaaaaaaa aa 1532

<210> 151  
<211> 226  
<212> PRT  
<213> Homo sapiens

<400> 151  
Met Glu Thr Val Val Ile Val Ala Ile Gly Val Leu Ala Thr Ile  
1 5 10 15  
Phe Leu Ala Ser Phe Ala Ala Leu Val Leu Val Cys Arg Gln Arg  
20 25 30  
Tyr Cys Arg Pro Arg Asp Leu Leu Gln Arg Tyr Asp Ser Lys Pro

	35	40	45
Ile Val Asp Leu	Ile Gly Ala Met Glu Thr Gln Ser Glu Pro Ser		
	50	55	60
Glu Leu Glu Leu Asp Asp Val Val Ile Thr Asn Pro His Ile Glu		70	75
	65		
Ala Ile Leu Glu Asn Glu Asp Trp Ile Glu Asp Ala Ser Gly Leu		85	90
	80		
Met Ser His Cys Ile Ala Ile Leu Lys Ile Cys His Thr Leu Thr		100	105
	95		
Glu Lys Leu Val Ala Met Thr Met Gly Ser Gly Ala Lys Met Lys		115	120
	110		
Thr Ser Ala Ser Val Ser Asp Ile Ile Val Val Ala Lys Arg Ile		130	135
	125		
Ser Pro Arg Val Asp Asp Val Val Lys Ser Met Tyr Pro Pro Leu		145	150
	140		
Asp Pro Lys Leu Leu Asp Ala Arg Thr Thr Ala Leu Leu Leu Ser		160	165
	155		
Val Ser His Leu Val Leu Val Thr Arg Asn Ala Cys His Leu Thr		175	180
	170		
Gly Gly Leu Asp Trp Ile Asp Gln Ser Leu Ser Ala Ala Glu Glu		190	195
	185		
His Leu Glu Val Leu Arg Glu Ala Ala Leu Ala Ser Glu Pro Asp		205	210
	200		
Lys Gly Leu Pro Gly Pro Glu Gly Phe Leu Gln Glu Gln Ser Ala		220	225
	215		
Ile			

<210> 152  
 <211> 1027  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 1017, 1020  
 <223> unknown base

<400> 152  
 gcttcatttc tcccgaactca gcttcccacc ctgggctttc cgaggtgctt 50  
 tcgccgctgt cccaccact gcagccatga tctccttaac ggacacgcag 100  
 aaaattggaa tgggattaac aggatttgga gtgtttttcc tggtctttgg 150  
 aatgattctc ttttttgaca aagcactact ggctattgga aatgttttat 200  
 ttgtagccgg cttggctttt gtaattgggt tagaaagaac attcagattc 250  
 ttcttccaaa aacataaaat gaaagotaca gggttttttc tgggtggtgt 300

attttagtagtc cttattgggtt ggcctttgat aggcattgatc ttcgaaattt 350  
 atggattttt tctcttggtt aggggcttct ttcctgtcgt tgttggcttt 400  
 attagaagag tgccagtcct tggatccctc ctaaatttac ctggaattag 450  
 atcatttgta gataaagttg gagaaagcaa caatatggta taacaacaag 500  
 tgaatttgaa gactcattta aaatattgtg ttatttataa agtcatttga 550  
 agaattattca gcacaaaatt aaattacatg aaatagcttg taatgttctt 600  
 tacaggagtt taaaacgtat agcctacaaa gtaccagcag caaattagca 650  
 aagaagcagt gaaaacaggc ttctactcaa gtgaactaag aagaagtcag 700  
 caagcaaact gagagaggtg aaatccatgt taatgatgct taagaaactc 750  
 ttgaaggcta tttgtgttgt ttttccacaa tgtgcgaaac tcagccatcc 800  
 ttagagaact gtggtgcctg tttcttttct ttttattttg aaggctcagg 850  
 agcatccata ggcatttgct ttttagaagt gtccactgca atggcaaaaa 900  
 tatttccagt tgcaactgtat ctctggaagt gatgcatgaa ttcgattgga 950  
 ttgtgtcatt ttaaagtatt aaaaccaagg aaacccaat tttgatgtat 1000  
 ggattacttt tttttgngcn cagggcc 1027

<210> 153  
 <211> 138  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> N-myristoylation Sites  
 <222> 11-16, 51-56 and 116-121  
 <223> N-myristoylation Sites.

<220>  
 <221> Transmembrane domains  
 <222> 12-30, 33-52, 69-89 and 93-109  
 <223> Transmembrane domains

<220>  
 <221> Aminoacyl-transfer RNA Synthetases.  
 <222> 49-59  
 <223> Aminoacyl-transfer RNA synthetases class-II protein.

<400> 153  
 Met Ile Ser Leu Thr Asp Thr Gln Lys Ile Gly Met Gly Leu Thr  
 1 5 10 15  
 Gly Phe Gly Val Phe Phe Leu Phe Phe Gly Met Ile Leu Phe Phe  
 20 25 30  
 Asp Lys Ala Leu Leu Ala Ile Gly Asn Val Leu Phe Val Ala Gly  
 35 40 45  
 Leu Ala Phe Val Ile Gly Leu Glu Arg Thr Phe Arg Phe Phe Phe  
 50 55 60



Gln Lys His Lys Met Lys Ala Thr Gly Phe Phe Leu Gly Gly Val  
65 70 75  
Phe Val Val Leu Ile Gly Trp Pro Leu Ile Gly Met Ile Phe Glu  
80 85 90  
Ile Tyr Gly Phe Phe Leu Leu Phe Arg Gly Phe Phe Pro Val Val  
95 100 105  
Val Gly Phe Ile Arg Arg Val Pro Val Leu Gly Ser Leu Leu Asn  
110 115 120  
Leu Pro Gly Ile Arg Ser Phe Val Asp Lys Val Gly Glu Ser Asn  
125 130 135  
Asn Met Val

<210> 154  
<211> 405  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 66  
<223> unknown base

<400> 154  
gaagacgtgg cggtctctgc ctgggctgtt tcccggttc atttctcccg 50  
actcagcttc ccacntggg ctttccgagg tgctttcgcc gctgtcccca 100  
ccactgcagc catgatctcc ttaacggaca cgcagaaaat tggaatggga 150  
ttaaccggat ttggagtgtt tttcctgttc tttggaatga ttctcttttt 200  
tgacaaagca ctactggcta ttggaaatgt tttatttgta gccggcttgg 250  
cttttgtaat tggtttagaa agaacattca gattcttctt ccaaaaacat 300  
aaaatgaaag ctacagggtt ttttctgggt ggtgtatttg tagtccttat 350  
tggttggcct ttgataggca tgatcttcga aatttatgga ttttttctct 400  
tgttc 405

<210> 155  
<211> 1781  
<212> DNA  
<213> Homo sapiens

<400> 155  
ggcacgaggc tgaaccagc cggtccatc tcagcttctg gtttctaagt 50  
ccatgtgcca aaggctgcca ggaaggagac gccttcctga gtcttgatc 100  
tttcttcctt ctggaaatct ttgactgtgg gtagttattt atttctgaat 150  
aagagcgtcc aogcatcatg gacctcgcg gactgctgaa gtctcagttc 200  
ctgtgccacc tggctctctg ctacgtcttt attgcctcag ggctaatacat 250

caacaccatt cagctcttca ctctcctcct ctggcccatt aacaagcagc 300  
 tcttccggaa gatcaactgc agactgtcct attgcatctc aagccagctg 350  
 gtgatgctgc tggagtgggtg gtogggcacg gaatgcacca tcttcacgga 400  
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<210> 156

[illegible]

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Ser Leu Val Leu	Tyr Pro Phe Phe Gln	Phe Leu Val Ser Met	Ile		
	320	325	330		
Arg Ser Gly Ser	Ser Leu Thr Leu Ala	Ser Phe Ile Leu Val	Phe		
	335	340	345		
Phe Val Ala Ser	Val Gly Val Arg Trp	Met Ile Gly Val Thr	Glu		
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Ile Asp Lys Gly	Ser Ala Tyr Gly Asn	Ser Asp Ser Lys Gln	Lys		
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Leu Asn Asp					

<210> 157  
 <211> 1849  
 <212> DNA  
 <213> Homo sapiens

<400> 157  
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Ser	Asp	Gln	Ile	Met	Thr	Phe	Arg	Glu	Arg	Leu	Leu	His	Lys	Asn	
				110					115					120	
Leu	Gln	Glu	His	Phe	Ser	Asn	Gln	Asp	Leu	Val	Phe	Leu	Leu	Leu	
				125					130					135	
Thr	Pro	Ser	Ile	Ile	Thr	Glu	Ser	Cys	Ser	Thr	His	Arg	Leu	Glu	
				140					145					150	
His	Ser	Leu	Tyr	Lys	Pro	Gln	Lys	Gly	Leu	Phe	His	Arg	Val	Pro	
				155					160					165	
Leu	Val	Val	Ala	Asn	Leu	Gly	Met	Ser	Glu	Gln	Leu	Gly	Tyr	Lys	
				170					175					180	
Thr	Val	Ser	Gly	Ser	Cys	Met	Ser	Thr	Gly	Phe	Ser	Arg	Ala	Val	
				185					190					195	
Gln	Thr	His	Ser	Ser	Lys	Phe	Phe	Glu	Glu	Asp	Gly	Ser	Leu	Lys	
				200					205					210	
Glu	Val	His	Lys	Ile	Asn	Glu	Met	Tyr	Ala	Ser	Leu	Gln	Glu	Glu	
				215					220					225	
Leu	Lys	Ser	Ile	Cys	Lys	Lys	Val	Glu	Asp	Ser	Glu	Gln	Ala	Val	
				230					235					240	
Asp	Lys	Leu	Val	Lys	Asp	Val	Asn	Arg	Leu	Lys	Arg	Glu	Ile	Glu	
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Lys	Arg	Arg	Gly	Ala	Gln	Ile	Gln	Ala	Ala	Arg	Glu	Lys	Asn	Ile	
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Gln	Lys	Asp	Pro	Gln	Glu	Asn	Ile	Phe	Leu	Cys	Gln	Ala	Leu	Arg	
				275					280					285	
Thr	Phe	Phe	Pro	Asn	Ser	Glu	Phe	Leu	His	Ser	Cys	Val	Met	Ser	
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Leu	Lys	Asn	Arg	His	Val	Ser	Lys	Ser	Ser	Cys	Asn	Tyr	Asn	His	
				305					310					315	
His	Leu	Asp	Val	Val	Asp	Asn	Leu	Thr	Leu	Met	Val	Glu	His	Thr	
				320					325					330	
Asp	Ile	Pro	Glu	Ala	Ser	Pro	Ala	Ser	Thr	Pro	Gln	Ile	Ile	Lys	
				335					340					345	
His	Lys	Ala	Leu	Asp	Leu	Asp	Asp	Arg	Trp	Gln	Phe	Lys	Arg	Ser	
				350					355					360	
Arg	Leu	Leu	Asp	Thr	Gln	Asp	Lys	Arg	Ser	Lys	Ala	Asn	Thr	Gly	
				365					370					375	
Ser	Ser	Asn	Gln	Asp	Lys	Ala	Ser	Lys	Met	Ser	Ser	Pro	Glu	Thr	
				380					385					390	
Asp	Glu	Glu	Ile	Glu	Lys	Met	Lys	Gly	Phe	Gly	Glu	Tyr	Ser	Arg	
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Ser	Pro	Thr	Phe												

<210> 159  
 <211> 2651  
 <212> DNA  
 <213> Homo sapiens

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<210> 160
<211> 556
<212> PRT
<213> Homo sapiens
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Ser Leu Gln Ser Lys Asp Asp Phe Lys Ser Val Val Ser Glu Gln	80	85	90
Cys Asn His Leu Gln Ala Val Phe Ala Ser Arg Tyr Lys Lys Phe	95	100	105
Asp Glu Phe Phe Lys Glu Leu Leu Glu Asn Ala Glu Lys Ser Leu	110	115	120
Asn Asp Met Phe Val Lys Thr Tyr Gly His Leu Tyr Met Gln Asn	125	130	135
Ser Glu Leu Phe Lys Asp Leu Phe Val Glu Leu Lys Arg Tyr Tyr	140	145	150
Val Val Gly Asn Val Asn Leu Glu Glu Met Leu Asn Asp Phe Trp	155	160	165
Ala Arg Leu Leu Glu Arg Met Phe Arg Leu Val Asn Ser Gln Tyr	170	175	180
His Phe Thr Asp Glu Tyr Leu Glu Cys Val Ser Lys Tyr Thr Glu	185	190	195
Gln Leu Lys Pro Phe Gly Asp Val Pro Arg Lys Leu Lys Leu Gln	200	205	210
Val Thr Arg Ala Phe Val Ala Ala Arg Thr Phe Ala Gln Gly Leu	215	220	225
Ala Val Ala Gly Asp Val Val Ser Lys Val Ser Val Val Asn Pro	230	235	240
Thr Ala Gln Cys Thr His Ala Leu Leu Lys Met Ile Tyr Cys Ser	245	250	255
His Cys Arg Gly Leu Val Thr Val Lys Pro Cys Tyr Asn Tyr Cys	260	265	270
Ser Asn Ile Met Arg Gly Cys Leu Ala Asn Gln Gly Asp Leu Asp	275	280	285
Phe Glu Trp Asn Asn Phe Ile Asp Ala Met Leu Met Val Ala Glu	290	295	300
Arg Leu Glu Gly Pro Phe Asn Ile Glu Ser Val Met Asp Pro Ile	305	310	315
Asp Val Lys Ile Ser Asp Ala Ile Met Asn Met Gln Asp Asn Ser	320	325	330
Val Gln Val Ser Gln Lys Val Phe Gln Gly Cys Gly Pro Pro Lys	335	340	345
Pro Leu Pro Ala Gly Arg Ile Ser Arg Ser Ile Ser Glu Ser Ala			

	350		355		360
Phe Ser Ala Arg	Phe Arg Pro His His	Pro Glu Glu Arg Pro	Thr		
	365	370	375		
Thr Ala Ala Gly	Thr Ser Leu Asp Arg	Leu Val Thr Asp Val	Lys		
	380	385	390		
Glu Lys Leu Lys	Gln Ala Lys Lys Phe	Trp Ser Ser Leu Pro	Ser		
	395	400	405		
Asn Val Cys Asn	Asp Glu Arg Met Ala	Ala Gly Asn Gly Asn	Glu		
	410	415	420		
Asp Asp Cys Trp	Asn Gly Lys Gly Lys	Ser Arg Tyr Leu Phe	Ala		
	425	430	435		
Val Thr Gly Asn	Gly Leu Ala Asn Gln	Gly Asn Asn Pro Glu	Val		
	440	445	450		
Gln Val Asp Thr	Ser Lys Pro Asp Ile	Leu Ile Leu Arg Gln	Ile		
	455	460	465		
Met Ala Leu Arg	Val Met Thr Ser Lys	Met Lys Asn Ala Tyr	Asn		
	470	475	480		
Gly Asn Asp Val	Asp Phe Phe Asp Ile	Ser Asp Glu Ser Ser	Gly		
	485	490	495		
Glu Gly Ser Gly	Ser Gly Cys Glu Tyr	Gln Gln Cys Pro Ser	Glu		
	500	505	510		
Phe Asp Tyr Asn	Ala Thr Asp His Ala	Gly Lys Ser Ala Asn	Glu		
	515	520	525		
Lys Ala Asp Ser	Ala Gly Val Arg Pro	Gly Ala Gln Ala Tyr	Leu		
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Leu Thr Val Phe	Cys Ile Leu Phe Leu	Val Met Gln Arg Glu	Trp		
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Arg

<210> 161  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 161  
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<210> 162  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 162  
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<210> 163  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 163  
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<210> 164  
<211> 870  
<212> DNA  
<213> Homo sapiens

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<210> 165  
<211> 119  
<212> PRT  
<213> Homo sapiens

<400> 165  
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Leu Met Ser Met Val Ser Ser Ser Leu Asn Pro Gly Val Ala Arg	20	25	30
Gly His Arg Asp Arg Gly Gln Ala Ser Arg Arg Trp Leu Gln Glu	35	40	45
Gly Gly Gln Glu Cys Glu Cys Lys Asp Trp Phe Leu Arg Ala Pro	50	55	60
Arg Arg Lys Phe Met Thr Val Ser Gly Leu Pro Lys Lys Gln Cys	65	70	75
Pro Cys Asp His Phe Lys Gly Asn Val Lys Lys Thr Arg His Gln	80	85	90
Arg His His Arg Lys Pro Asn Lys His Ser Arg Ala Cys Gln Gln	95	100	105
Phe Leu Lys Gln Cys Gln Leu Arg Ser Phe Ala Leu Pro Leu	110	115	

<210> 166  
 <211> 551  
 <212> DNA  
 <213> Homo sapiens

<400> 166  
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 tccaagagca gccaaatcct gcttttccag tttgggtcca caagtcctcc 350  
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 agaggaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 550  
 a 551

<210> 167  
 <211> 87  
 <212> PRT  
 <213> Homo sapiens

<400> 167  
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Asp Asp Lys Pro	Asp Asp Ser Gly Lys Asp Pro Lys Pro Asp Phe				
	35		40		45
Pro Lys Phe Leu Ser Leu Leu Gly Thr Glu Ile Ile Glu Asn Ala					
	50		55		60
Val Glu Phe Ile Leu Arg Ser Met Ser Arg Ser Thr Gly Phe Met					
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Glu Phe Asp Asp Asn Glu Gly Lys His Ser Ser Lys					
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<210> 168  
 <211> 1371  
 <212> DNA  
 <213> Homo sapiens

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gcctcccaat gttgtccctt tccttcgttc ccatggtaaa gctcctctcg 1150  
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<210> 169  
 <211> 277  
 <212> PRT  
 <213> Homo sapiens

<400> 169  
 Met Asp Ile Leu Val Pro Leu Leu Gln Leu Leu Val Leu Leu Leu  
 1 5 10 15  
 Thr Leu Pro Leu His Leu Met Ala Leu Leu Gly Cys Trp Gln Pro  
 20 25 30  
 Leu Cys Lys Ser Tyr Phe Pro Tyr Leu Met Ala Val Leu Thr Pro  
 35 40 45  
 Lys Ser Asn Arg Lys Met Glu Ser Lys Lys Arg Glu Leu Phe Ser  
 50 55 60  
 Gln Ile Lys Gly Leu Thr Gly Ala Ser Gly Lys Val Ala Leu Leu  
 65 70 75  
 Glu Leu Gly Cys Gly Thr Gly Ala Asn Phe Gln Phe Tyr Pro Pro  
 80 85 90  
 Gly Cys Arg Val Thr Cys Leu Asp Pro Asn Pro His Phe Glu Lys  
 95 100 105  
 Phe Leu Thr Lys Ser Met Ala Glu Asn Arg His Leu Gln Tyr Glu  
 110 115 120  
 Arg Phe Val Val Ala Pro Gly Glu Asp Met Arg Gln Leu Ala Asp  
 125 130 135  
 Gly Ser Met Asp Val Val Val Cys Thr Leu Val Leu Cys Ser Val  
 140 145 150  
 Gln Ser Pro Arg Lys Val Leu Gln Glu Val Arg Arg Val Leu Arg  
 155 160 165  
 Pro Gly Gly Val Leu Phe Phe Trp Glu His Val Ala Glu Pro Tyr  
 170 175 180  
 Gly Ser Trp Ala Phe Met Trp Gln Gln Val Phe Glu Pro Thr Trp  
 185 190 195  
 Lys His Ile Gly Asp Gly Cys Cys Leu Thr Arg Glu Thr Trp Lys  
 200 205 210  
 Asp Leu Glu Asn Ala Gln Phe Ser Glu Ile Gln Met Glu Arg Gln  
 215 220 225

Pro Pro Pro Leu Lys Trp Leu Pro Val Gly Pro His Ile Met Gly  
 230 235 240  
 Lys Ala Val Lys Gln Ser Phe Pro Ser Ser Lys Ala Leu Ile Cys  
 245 250 255  
 Ser Phe Pro Ser Leu Gln Leu Glu Gln Ala Thr His Gln Pro Ile  
 260 265 270  
 Tyr Leu Pro Leu Arg Gly Thr  
 275

<210> 170  
 <211> 1621  
 <212> DNA  
 <213> Homo sapiens

<400> 170  
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 cctcatcgca ggcagatggt ggggctttgt ccgaacagct cccctctgcc 100  
 agcttctgta gataaggggt aaaaactaat atttatatga cagaagaaaa 150  
 agatgtcatt ccgtaaagta aacatcatca tcttggtcct ggctgttgct 200  
 ctcttcttac tggttttgca ccataacttc ctcagcttga gcagtttggt 250  
 aaggaatgag gttacagatt caggaattgt agggcctcaa cctatagact 300  
 ttgtcccaaa tgctctccga catgcagtag atgggagaca agaggagatt 350  
 cctgtggtca tcgctgcac tgaagacagg cttggggggg ccattgcagc 400  
 tataaacagc attcagcaca aactcgctc caatgtgatt ttctacattg 450  
 ttactctcaa caatacagca gaccatctcc ggtcctggct caacagtgat 500  
 tcctgaaaa gcatcagata caaattgtc aattttgacc ctaaaactttt 550  
 ggaaggaaaa gtaaaggagg atcctgacca gggggaatcc atgaaacctt 600  
 taacctttgc aaggttctac ttgccaattc tggttcccag cgcaaagaag 650  
 gccatataca tggatgatga tgtaattgtg caaggtgata ttcttgccct 700  
 ttacaatata gcactgaagc caggacatgc agctgcattt tcagaagatt 750  
 gtgattcagc ctctactaaa gttgtcatcc gtggagcagg aaaccagtac 800  
 aattacattg gctatcttga ctataaaaag gaaagaattc gtaagctttc 850  
 catgaaagcc agcacttgct catttaatcc tggagttttt gttgcaaacc 900  
 tgacggaatg gaaacgacag aatataacta accaactgga aaaatggatg 950  
 aaactcaatg tagaagaggg actgtatagc agaaccctgg ctggtagcat 1000  
 cacaacacct cctctgctta tcgtatttta tcaacagcac tctaccatcg 1050  
 atcctatgtg gaatgtccgc caccttggtt ccagtgtgtg aaaacgatat 1100  
 tcacctcagt ttgtaaaggc tgccaagtta ctccattgga atggacattt 1150

gaagccatgg ggaaggactg cttcatatac tgatgtttgg gaaaaatggg 1200  
atattccaga cccaacaggc aaattcaacc taatccgaag atataccgag 1250  
atctcaaaca taaagtgaaa cagaatttga actgtaagca agcattttctc 1300  
aggaagtcct ggaagatagc atgcatggga agtaacagtt gctaggcttc 1350  
aatgcctatc ggtagcaagc catggaaaaa gatgtgtcag ctaggtaaag 1400  
atgacaaaact gccctgtctg gcagtcagct tcccagacag actatagact 1450  
ataaatatgt ctccatctgc cttaccaagt gttttcttac tacaatgctg 1500  
aatgactgga aagaagaact gatatggcta gttcagctag ctggtacaga 1550  
taattcaaaa ctgctgttgg ttttaatttt gtaacctgtg gcctgatctg 1600  
taaataaaac ttacattttt c 1621

<210> 171  
<211> 371  
<212> PRT  
<213> Homo sapiens

<400> 171  
Met Ser Phe Arg Lys Val Asn Ile Ile Ile Leu Val Leu Ala Val  
1 5 10 15  
Ala Leu Phe Leu Leu Val Leu His His Asn Phe Leu Ser Leu Ser  
20 25 30  
Ser Leu Leu Arg Asn Glu Val Thr Asp Ser Gly Ile Val Gly Pro  
35 40 45  
Gln Pro Ile Asp Phe Val Pro Asn Ala Leu Arg His Ala Val Asp  
50 55 60  
Gly Arg Gln Glu Glu Ile Pro Val Val Ile Ala Ala Ser Glu Asp  
65 70 75  
Arg Leu Gly Gly Ala Ile Ala Ala Ile Asn Ser Ile Gln His Asn  
80 85 90  
Thr Arg Ser Asn Val Ile Phe Tyr Ile Val Thr Leu Asn Asn Thr  
95 100 105  
Ala Asp His Leu Arg Ser Trp Leu Asn Ser Asp Ser Leu Lys Ser  
110 115 120  
Ile Arg Tyr Lys Ile Val Asn Phe Asp Pro Lys Leu Leu Glu Gly  
125 130 135  
Lys Val Lys Glu Asp Pro Asp Gln Gly Glu Ser Met Lys Pro Leu  
140 145 150  
Thr Phe Ala Arg Phe Tyr Leu Pro Ile Leu Val Pro Ser Ala Lys  
155 160 165  
Lys Ala Ile Tyr Met Asp Asp Asp Val Ile Val Gln Gly Asp Ile  
170 175 180  
Leu Ala Leu Tyr Asn Thr Ala Leu Lys Pro Gly His Ala Ala Ala



	185		190		195
Phe Ser Glu Asp	Cys Asp Ser Ala Ser	Thr Lys Val Val Ile	Arg		
	200	205	210		
Gly Ala Gly Asn	Gln Tyr Asn Tyr Ile	Gly Tyr Leu Asp Tyr	Lys		
	215	220	225		
Lys Glu Arg Ile	Arg Lys Leu Ser Met	Lys Ala Ser Thr Cys	Ser		
	230	235	240		
Phe Asn Pro Gly	Val Phe Val Ala Asn	Leu Thr Glu Trp Lys	Arg		
	245	250	255		
Gln Asn Ile Thr	Asn Gln Leu Glu Lys	Trp Met Lys Leu Asn	Val		
	260	265	270		
Glu Glu Gly Leu	Tyr Ser Arg Thr Leu	Ala Gly Ser Ile Thr	Thr		
	275	280	285		
Pro Pro Leu Leu	Ile Val Phe Tyr Gln	Gln His Ser Thr Ile	Asp		
	290	295	300		
Pro Met Trp Asn	Val Arg His Leu Gly	Ser Ser Ala Gly Lys	Arg		
	305	310	315		
Tyr Ser Pro Gln	Phe Val Lys Ala Ala	Lys Leu Leu His Trp	Asn		
	320	325	330		
Gly His Leu Lys	Pro Trp Gly Arg Thr	Ala Ser Tyr Thr Asp	Val		
	335	340	345		
Trp Glu Lys Trp	Tyr Ile Pro Asp Pro	Thr Gly Lys Phe Asn	Leu		
	350	355	360		
Ile Arg Arg Tyr	Thr Glu Ile Ser Asn	Ile Lys			
	365	370			

<210> 172  
 <211> 585  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 71, 76, 86, 91, 162, 220, 269, 281  
 <223> unknown base

<400> 172  
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 aggttacaga ttcaggaatt ntaggncctc aacctntaga ntttgtccca 100  
 aatgtttctcc gacatgcagt agatgggaga caagaggaga ttcctgtggt 150  
 catcgctgca tntgaagaca ggcttggggg ggccattgca gctataaaca 200  
 gcattcagca caacactcgn tccaatgtga ttttctacat tgttactctc 250  
 aacaatacag cagaccatnt ccggtcctgg ntcaacagtg attccctgaa 300  
 aagcatcaga tacaaaattg tcaattttga ccctaaactt ttggaaggaa 350

aagtaaagga ggatcctgac cagggggaat ccatgaaacc tttaaccttt 400  
gcaaggttct acttgccaat tctggttccc agcgcaaaga aggccatata 450  
catggatgat gatgtaattg tgcaaggtga tattcttgcc ctttacaata 500  
cagcactgaa gccaggacat gcagctgcat tttcagaaga ttgtgattca 550  
gccttacta aagttgtcat ccgtggagca ggaaa 585

<210> 173  
<211> 1866  
<212> DNA  
<213> Homo sapiens

<400> 173  
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gcggctgcca cggagctaga gggcaagtgt gctcggccca gcgtgcaggg 100  
aacgcgggcg gccagacaac gggctgggct ccggggcctg cggcgcgggc 150  
gctgagctgg cagggcgggt cggggcgcg gctgcatccg catctcctcc 200  
atgcctgca gtaagggcgg ccgcggcgag cctttgaggg gaacgacttg 250  
tcggagccct aaccaggggt gtctctgagc ctggtgggat ccccgagcgc 300  
tcacatcact ttccgatcac ttcaaagtgg ttaaaaacta atatttatat 350  
gacagaagaa aaagatgtca ttccgtaaag taaacatcat catcttggtc 400  
ctgggctggt gctctcttct tactggtttt gcaccataac ttctcagct 450  
tgaggcagtt tgttaaggaa tgaggttaca gattcaggaa ttgtagggcc 500  
tcaacctata ggactttgtc ccaaagtctc tccgacatgc agtagatggg 550  
agacaagagg agattcctgt ggtcatcgct gcattctgaag acaggcttgg 600  
gggggccatt gcagctataa acagcattca gcacaacact cgctccaatg 650  
tgattttcta cattgttact ctcaacaata cagcagacca tctccgggtc 700  
tgggctcaac agtgattccc tgaaaagcat cagatacaaa attgtcaatt 750  
ttgaccctaa acttttgaa ggaaaagtaa aggaggatcc tgaccagggg 800  
gaatccatga aacctttaac ctttgcaagg ttctacttgc caattctggg 850  
ttcccagcgc aaagaaggcc atatacatgg atgatgatgt aattgtgcaa 900  
ggtgatattc ttgcccttta caatacagca ctgaagccag gacatgcagc 950  
tgcattttca gaagattgtg attcagcctc tactaaagtt gtcattccgtg 1000  
gagcaggaaa ccagtacaat tacattggct atcttgacta taaaaggaa 1050  
agaattcgta agctttccat gaaagccagc acttgctcat ttaatcctgg 1100  
agtttttgtt gcaaacctga cggaatggaa acgacagaat ataactaacc 1150  
aactggaaaa atggatgaaa ctcaatgtag aagagggact gtatagcaga 1200

accctggctg	gtagcatcac	aacacctcct	ctgcttatcg	tattttatca	1250
acagcactct	accatcgatc	ctatgtggaa	tgtccgccac	cttggttcca	1300
gtgctggaaa	acgatattca	cctcagtttg	taaaggctgc	caagttactc	1350
cattggaatg	gacatttgaa	gccatgggga	aggactgctt	catatactga	1400
tgtttgggga	aaaatgggat	attccagacc	caacaggcaa	attcaaccta	1450
atccgaagat	ataccgagat	ctcaaacata	aagtgaaaca	gaatttgaac	1500
tgtaagcaag	catttctcag	gaagtcctgg	aagatagcat	gcgtgggaag	1550
taacagttgc	taggcttcaa	tgcttatcgg	tagcaagcca	tggaaaaaga	1600
tgtgtcagct	aggtaaagat	gacaaactgc	cctgtctggc	agtcagcttc	1650
ccagacagac	tatagactat	aaatatgtct	ccatctgcct	taccaagtgt	1700
tttcttacta	caatgctgaa	tgactggaaa	gaagaactga	tatggctagt	1750
tcagctagct	ggtacagata	attcaaaact	gctgttggtt	ttaattttgt	1800
aacctgtggc	ctgatctgta	aataaaaactt	acatttttca	ataggtaaaa	1850
aaaaaaaaaa	aaaaaa				1866

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<210> 174
<211> 823
<212> DNA
<213> Homo sapiens
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ctgtgccagca	aatgactata	gctggggcag	tggttacttg	ttatttcaac	800
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tctcttcttc	taccatcaag	gaaccgttgt	gaaagggtca	tttttaatat	900
ctgtggtgag	gattccgaga	atcattgtca	tgtacatgca	aaacgcactg	950
aaagaacagc	agcatggtgc	attgtccagg	tacctgttcc	gatgctgcta	1000
ctgctgtttc	tgggtgtcttg	acaaatacct	gctccatctc	aaccagaatg	1050
catatactac	aactgctatt	aatgggacag	atttctgtac	atcagcaaaa	1100
gatgcattca	aaatcttgtc	caagaactca	agtcacttta	catctattaa	1150
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tcactgtttt	tggaggactc	atggccttta	actacaatcg	ggcattccag	1250
gtgtgggcag	tccctctggt	attggtagct	ttttttgcct	acttagtagc	1300
ccatagtttt	ttatctgtgt	ttgaaactgt	gctggatgca	cttttcctgt	1350
gttttgctgt	tgatctggaa	acaaatgatg	gatcgtcaga	aaagccctac	1400
tttatggatc	agaattttct	gagtttcgta	aaaaggagca	acaaattaaa	1450
caatgcaagg	gcacagcagg	acaagcactc	attaaggaat	gaggagggaa	1500
cagaactcca	ggccattgtg	agatagatac	ccatttaggt	atctgtacct	1550
ggaaaacatt	tccttctaag	agccattttac	agaatagaag	atgagaccac	1600
tagagaaaag	ttagtgaatt	tttttttaaa	agaccttaata	aaccctattc	1650
ttcctcaaaa	1660				

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<210> 177
<211> 445
<212> PRT
<213> Homo sapiens
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<400> 177														
Met	Ser	Gly	Arg	Asp	Thr	Ile	Leu	Gly	Leu	Cys	Ile	Leu	Ala	Leu
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Ala	Leu	Ser	Leu	Ala	Met	Met	Phe	Thr	Phe	Arg	Phe	Ile	Thr	Thr
				20					25					30
Leu	Leu	Val	His	Ile	Phe	Ile	Ser	Leu	Val	Ile	Leu	Gly	Leu	Leu
				35					40					45
Phe	Val	Cys	Gly	Val	Leu	Trp	Trp	Leu	Tyr	Tyr	Asp	Tyr	Thr	Asn
				50					55					60
Asp	Leu	Ser	Ile	Glu	Leu	Asp	Thr	Glu	Arg	Glu	Asn	Met	Lys	Cys
				65					70					75
Val	Leu	Gly	Phe	Ala	Ile	Val	Ser	Thr	Gly	Ile	Thr	Ala	Val	Leu
				80					85					90
Leu	Val	Leu	Ile	Phe	Val	Leu	Arg	Lys	Arg	Ile	Lys	Leu	Thr	Val

95										100					105				
Glu	Leu	Phe	Gln	Ile	Thr	Asn	Lys	Ala	Ile	Ser	Ser	Ala	Pro	Phe					
				110					115					120					
Leu	Leu	Phe	Gln	Pro	Leu	Trp	Thr	Phe	Ala	Ile	Leu	Ile	Phe	Phe					
				125					130					135					
Trp	Val	Leu	Trp	Val	Ala	Val	Leu	Leu	Ser	Leu	Gly	Thr	Ala	Gly					
				140					145					150					
Ala	Ala	Gln	Val	Met	Glu	Gly	Gly	Gln	Val	Glu	Tyr	Lys	Pro	Leu					
				155					160					165					
Ser	Gly	Ile	Arg	Tyr	Met	Trp	Ser	Tyr	His	Leu	Ile	Gly	Leu	Ile					
				170					175					180					
Trp	Thr	Ser	Glu	Phe	Ile	Leu	Ala	Cys	Gln	Gln	Met	Thr	Ile	Ala					
				185					190					195					
Gly	Ala	Val	Val	Thr	Cys	Tyr	Phe	Asn	Arg	Ser	Lys	Asn	Asp	Pro					
				200					205					210					
Pro	Asp	His	Pro	Ile	Leu	Ser	Ser	Leu	Ser	Ile	Leu	Phe	Phe	Tyr					
				215					220					225					
His	Gln	Gly	Thr	Val	Val	Lys	Gly	Ser	Phe	Leu	Ile	Ser	Val	Val					
				230					235					240					
Arg	Ile	Pro	Arg	Ile	Ile	Val	Met	Tyr	Met	Gln	Asn	Ala	Leu	Lys					
				245					250					255					
Glu	Gln	Gln	His	Gly	Ala	Leu	Ser	Arg	Tyr	Leu	Phe	Arg	Cys	Cys					
				260					265					270					
Tyr	Cys	Cys	Phe	Trp	Cys	Leu	Asp	Lys	Tyr	Leu	Leu	His	Leu	Asn					
				275					280					285					
Gln	Asn	Ala	Tyr	Thr	Thr	Thr	Ala	Ile	Asn	Gly	Thr	Asp	Phe	Cys					
				290					295					300					
Thr	Ser	Ala	Lys	Asp	Ala	Phe	Lys	Ile	Leu	Ser	Lys	Asn	Ser	Ser					
				305					310					315					
His	Phe	Thr	Ser	Ile	Asn	Cys	Phe	Gly	Asp	Phe	Ile	Ile	Phe	Leu					
				320					325					330					
Gly	Lys	Val	Leu	Val	Val	Cys	Phe	Thr	Val	Phe	Gly	Gly	Leu	Met					
				335					340					345					
Ala	Phe	Asn	Tyr	Asn	Arg	Ala	Phe	Gln	Val	Trp	Ala	Val	Pro	Leu					
				350					355					360					
Leu	Leu	Val	Ala	Phe	Phe	Ala	Tyr	Leu	Val	Ala	His	Ser	Phe	Leu					
				365					370					375					
Ser	Val	Phe	Glu	Thr	Val	Leu	Asp	Ala	Leu	Phe	Leu	Cys	Phe	Ala					
				380					385					390					
Val	Asp	Leu	Glu	Thr	Asn	Asp	Gly	Ser	Ser	Glu	Lys	Pro	Tyr	Phe					
				395					400					405					
Met	Asp	Gln	Glu	Phe	Leu	Ser	Phe	Val	Lys	Arg	Ser	Asn	Lys	Leu					

	410		415		420
Asn Asn Ala Arg	Ala Gln Gln Asp Lys His Ser Leu Arg Asn Glu				
	425		430		435
Glu Gly Thr Glu	Leu Gln Ala Ile Val Arg				
	440		445		

<210> 178  
 <211> 2773  
 <212> DNA  
 <213> Homo sapiens

<400> 178  
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 tgtttcttcc ttagaataat ttgtatggga tttgtgatgc aggaaagcct 100  
 aagggaaaaa gaatattcat tctgtgtggt gaaaattttt tgaaaaaaa 150  
 attgccttct tcaaacaagg gtgtcattct gatatttatg aggactgttg 200  
 ttctcactat gaaggcatct gttattgaaa tgttccttgt tttgctggtg 250  
 actggagtac attcaaacaa agaaacggca aagaagatta aaaggcccaa 300  
 gttcactgtg cctcagatca actgcatgtt caaagccgga aagatcatcg 350  
 atcctgagtt cattgtgaaa tgtccagcag gatgccaaga ccccaaatac 400  
 catgtttatg gcaactgacgt gtatgcatcc tactccagtg tgtgtggcgc 450  
 tgccgtacac agtgggtgtg ttgataattc aggagggaaa atacttggtc 500  
 ggaaggttgc tggacagtct gggtacaaag ggagttattc caacggtgtc 550  
 caatcggttat ccctaccacg atggagagaa tccttttatcg tcttagaaag 600  
 taaacccaaa aaggggtgtaa cctaccatc agctcttaca tactcatcat 650  
 cgaaaagtcc agctgcccaa gcaggtgaga ccacaaaagc ctatcagagg 700  
 ccacctattc cagggaacaac tgcacagccg gtcactctga tgcagcttct 750  
 ggctgtcact gtagctgtgg ccacccccac caccttgcca aggccatccc 800  
 cttctgctgc ttctaccacc agcatcccca gaccacaatc agtgggccac 850  
 aggagccagg agatggatct ctgggtccact gccacctaca caagcagcca 900  
 aaacaggccc agagctgatc caggtatcca aaggcaagat ccttcaggag 950  
 ctgccttcca gaaacctgtt ggagcggatg tcagcctggg acttggtcca 1000  
 aaagaagaat tgagcacaca gtctttggag ccagtatccc tgggagatcc 1050  
 aaactgcaaa attgacttgt cgtttttaat tgatgggagc accagcattg 1100  
 gcaaacggcg attccgaatc cagaagcagc tcctggctga tgttgcccaa 1150  
 gctcttgaca ttggccctgc cgggtccactg atgggtgttg tccagtatgg 1200  
 agacaaccct gctactcact ttaacctcaa gacacacacg aattctcgag 1250

atctgaagac agccatagag aaaattactc agagaggagg acttttcta 1300  
 gtaggtcggg ccatctcctt tgtgaccaag aacttctttt ccaaagccaa 1350  
 tggaaacaga agcggggctc ccaatgtggt ggtggtgatg gtggatggct 1400  
 ggccacgga caaagtggag gaggcttcaa gacttgcgag agagtcagga 1450  
 atcaacattt tcttcatcac cattgaaggt gctgctgaaa atgagaagca 1500  
 gtatgtggtg gagcccaact ttgcaaaca ggccgtgtgc agaacaacg 1550  
 gcttctactc gctccaagt gtagagctggt ttggcctcca caagaccctg 1600  
 cagcctctgg tgaagcgggt ctgcgacact gaccgcctgg cctgcagcaa 1650  
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 gtgtgggggac gggcaacttc cgcaccgtcc tccagtttgt gaccaacctc 1750  
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 gtacacctac gaacagcggc tggagtttgg gttcgacaag tacagcagca 1850  
 agcctgacat cctcaacgcc atcaagaggg tgggctactg gagtgggtggc 1900  
 accagcacgg gggctgccat caacttcgcc ctggagcagc tcttcaagaa 1950  
 gtccaagccc aacaagagga agttaatgat cctcatcacc gacgggaggt 2000  
 cctacgacga cgtccggatc ccagccatgg ctgcccattc gaagggagt 2050  
 atcacctatg cgataggcgt tgccctgggt gcccaagagg agctagaagt 2100  
 cattgccact caccocgcca gagaccactc cttctttgtg gacgagtttg 2150  
 acaacctcca tcagtatgtc ccaggatca tccagaacat ttgtacagag 2200  
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 gtgctgcttt actaactgac gtgttgacc accccaccgc ttaatggggc 2300  
 acgcacggtg catcaagtct tgggcagggc atggagaaac aaatgtcttg 2350  
 ttattattct ttgccatcat gctttttcat attccaaaac ttggagtta 2400  
 aaagatgac acaaacgtat agaatgagcc aaaaggctac atcatgttga 2450  
 ggggtgctgga gattttacat ttgacaatt gttttcaaaa taaatgttcg 2500  
 gaatacagt gagcccttac gacaggctta cgtagagctt ttgtgagatt 2550  
 tttagttgt tatttctgat ttgaactctg taaccctcag caagtttcat 2600  
 ttttgtcatg acaatgtagg aattgctgaa ttaaatgttt agaaggatga 2650  
 aaaataaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2700  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2750  
 aaaaaaaaaa aaaaaaaaaa aag 2773

<210> 179



<211> 678  
 <212> PRT  
 <213> Homo sapiens

<400> 179

Met	Arg	Thr	Val	Val	Leu	Thr	Met	Lys	Ala	Ser	Val	Ile	Glu	Met	1	5	10	15
Phe	Leu	Val	Leu	Leu	Val	Thr	Gly	Val	His	Ser	Asn	Lys	Glu	Thr	20	25	30	
Ala	Lys	Lys	Ile	Lys	Arg	Pro	Lys	Phe	Thr	Val	Pro	Gln	Ile	Asn	35	40	45	
Cys	Asp	Val	Lys	Ala	Gly	Lys	Ile	Ile	Asp	Pro	Glu	Phe	Ile	Val	50	55	60	
Lys	Cys	Pro	Ala	Gly	Cys	Gln	Asp	Pro	Lys	Tyr	His	Val	Tyr	Gly	65	70	75	
Thr	Asp	Val	Tyr	Ala	Ser	Tyr	Ser	Ser	Val	Cys	Gly	Ala	Ala	Val	80	85	90	
His	Ser	Gly	Val	Leu	Asp	Asn	Ser	Gly	Gly	Lys	Ile	Leu	Val	Arg	95	100	105	
Lys	Val	Ala	Gly	Gln	Ser	Gly	Tyr	Lys	Gly	Ser	Tyr	Ser	Asn	Gly	110	115	120	
Val	Gln	Ser	Leu	Ser	Leu	Pro	Arg	Trp	Arg	Glu	Ser	Phe	Ile	Val	125	130	135	
Leu	Glu	Ser	Lys	Pro	Lys	Lys	Gly	Val	Thr	Tyr	Pro	Ser	Ala	Leu	140	145	150	
Thr	Tyr	Ser	Ser	Ser	Lys	Ser	Pro	Ala	Ala	Gln	Ala	Gly	Glu	Thr	155	160	165	
Thr	Lys	Ala	Tyr	Gln	Arg	Pro	Pro	Ile	Pro	Gly	Thr	Thr	Ala	Gln	170	175	180	
Pro	Val	Thr	Leu	Met	Gln	Leu	Leu	Ala	Val	Thr	Val	Ala	Val	Ala	185	190	195	
Thr	Pro	Thr	Thr	Leu	Pro	Arg	Pro	Ser	Pro	Ser	Ala	Ala	Ser	Thr	200	205	210	
Thr	Ser	Ile	Pro	Arg	Pro	Gln	Ser	Val	Gly	His	Arg	Ser	Gln	Glu	215	220	225	
Met	Asp	Leu	Trp	Ser	Thr	Ala	Thr	Tyr	Thr	Ser	Ser	Gln	Asn	Arg	230	235	240	
Pro	Arg	Ala	Asp	Pro	Gly	Ile	Gln	Arg	Gln	Asp	Pro	Ser	Gly	Ala	245	250	255	
Ala	Phe	Gln	Lys	Pro	Val	Gly	Ala	Asp	Val	Ser	Leu	Gly	Leu	Val	260	265	270	
Pro	Lys	Glu	Glu	Leu	Ser	Thr	Gln	Ser	Leu	Glu	Pro	Val	Ser	Leu	275	280	285	
Gly	Asp	Pro	Asn	Cys	Lys	Ile	Asp	Leu	Ser	Phe	Leu	Ile	Asp	Gly				

	290		295		300
Ser Thr Ser Ile	Gly Lys Arg Arg Phe	Arg Ile Gln Lys Gln	Leu		
	305	310		315	
Leu Ala Asp Val	Ala Gln Ala Leu Asp	Ile Gly Pro Ala Gly	Pro		
	320	325		330	
Leu Met Gly Val	Val Gln Tyr Gly Asp	Asn Pro Ala Thr His	Phe		
	335	340		345	
Asn Leu Lys Thr	His Thr Asn Ser Arg	Asp Leu Lys Thr Ala	Ile		
	350	355		360	
Glu Lys Ile Thr	Gln Arg Gly Gly Leu	Ser Asn Val Gly Arg	Ala		
	365	370		375	
Ile Ser Phe Val	Thr Lys Asn Phe Phe	Ser Lys Ala Asn Gly	Asn		
	380	385		390	
Arg Ser Gly Ala	Pro Asn Val Val Val	Val Met Val Asp Gly	Trp		
	395	400		405	
Pro Thr Asp Lys	Val Glu Glu Ala Ser	Arg Leu Ala Arg Glu	Ser		
	410	415		420	
Gly Ile Asn Ile	Phe Phe Ile Thr Ile	Glu Gly Ala Ala Glu	Asn		
	425	430		435	
Glu Lys Gln Tyr	Val Val Glu Pro Asn	Phe Ala Asn Lys Ala	Val		
	440	445		450	
Cys Arg Thr Asn	Gly Phe Tyr Ser Leu	His Val Gln Ser Trp	Phe		
	455	460		465	
Gly Leu His Lys	Thr Leu Gln Pro Leu	Val Lys Arg Val Cys	Asp		
	470	475		480	
Thr Asp Arg Leu	Ala Cys Ser Lys Thr	Cys Leu Asn Ser Ala	Asp		
	485	490		495	
Ile Gly Phe Val	Ile Asp Gly Ser Ser	Ser Val Gly Thr Gly	Asn		
	500	505		510	
Phe Arg Thr Val	Leu Gln Phe Val Thr	Asn Leu Thr Lys Glu	Phe		
	515	520		525	
Glu Ile Ser Asp	Thr Asp Thr Arg Ile	Gly Ala Val Gln Tyr	Thr		
	530	535		540	
Tyr Glu Gln Arg	Leu Glu Phe Gly Phe	Asp Lys Tyr Ser Ser	Lys		
	545	550		555	
Pro Asp Ile Leu	Asn Ala Ile Lys Arg	Val Gly Tyr Trp Ser	Gly		
	560	565		570	
Gly Thr Ser Thr	Gly Ala Ala Ile Asn	Phe Ala Leu Glu Gln	Leu		
	575	580		585	
Phe Lys Lys Ser	Lys Pro Asn Lys Arg	Lys Leu Met Ile Leu	Ile		
	590	595		600	
Thr Asp Gly Arg	Ser Tyr Asp Asp Val	Arg Ile Pro Ala Met	Ala		

	605		610		615
Ala His Leu Lys	Gly Val Ile Thr Tyr	Ala Ile Gly Val Ala	Trp		
	620	625	630		
Ala Ala Gln Glu	Glu Leu Glu Val Ile	Ala Thr His Pro Ala	Arg		
	635	640	645		
Asp His Ser Phe	Phe Val Asp Glu Phe	Asp Asn Leu His Gln	Tyr		
	650	655	660		
Val Pro Arg Ile	Ile Gln Asn Ile Cys	Thr Glu Phe Asn Ser	Gln		
	665	670	675		

Pro Arg Asn

<210> 180  
 <211> 1759  
 <212> DNA  
 <213> Homo sapiens

<400> 180  
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 acacgagctc tatgcctttc cggctgctca tcccgcctcg cctcctgtgc 100  
 gcgctgctgc ctcagcacca tgggtgcgcca ggtcccgcgc gctccgcgcc 150  
 agatcccgcc cactacagtt tttctctgac tctaattgat gcaactggaca 200  
 ccttgctgat tttggggaat gtctcagaat tccaaagagt gggtgaagtg 250  
 ctccaggaca gcgtggactt tgatattgat gtgaacgcct ctgtgtttga 300  
 aacaaacatt cgagtggtag gaggactcct gtctgctcat ctgctctcca 350  
 agaaggctgg ggtggaagta gaggctggat ggccctgttc cgggcctctc 400  
 ctgagaatgg ctgaggaggc ggcccgaata ctctcccag cctttcagac 450  
 cccactggc atgcatatg gaacagtga cttacttcat ggcgtgaacc 500  
 caggagagac ccctgtcacc tgtacggcag ggattgggac cttcattgtt 550  
 gaatttgcca ccctgagcag cctcactggg gaccgggtgt tcgaagatgt 600  
 ggccagagtg gctttgatgc gcctctggga gagccgggtc gatatcgggc 650  
 tggtcggcaa ccacattgat gtgctcactg gcaagtgggt ggcccaggac 700  
 gcaggcatcg gggctggcgt ggactcctac tttgagtact tggtgaaagg 750  
 agccatcctg cttcaggata agaagctcat ggccatgttc ctagagtata 800  
 acaaagccat ccggaactac accgccttcg atgactggta cctgtggggt 850  
 cagatgtaca aggggactgt gtccatgcca gtcttccagt ccttgagggc 900  
 ctactggcct ggtcttcaga gcctcattgg agacattgac aatgccatga 950  
 ggaccttcct caactactac actgtatgga agcagtttgg ggggctcccg 1000

gaattctaca acattcctca gggatacaca gtggagaagc gagagggcta 1050  
 cccacttcgg ccagaactta ttgaaagcgc aatgtacctc taccgtgcc 1100  
 cgggggatcc caccctccta gaactoggaa gagatgctgt ggaatccatt 1150  
 gaaaaaatca gcaaggtgga gtgcggattt gcaacaatca aagatctgcg 1200  
 agaccacaag ctggacaacc gcatggagtc gttcttcctg gccgagactg 1250  
 tgaaatacct ctacctcctg tttagaccaa ccaacttcac ccacaacaat 1300  
 gggtcacact tcgacgcggg gatcaccccc tatggggagt gcatcctggg 1350  
 ggctgggggg tacatcttca acacagaagc tcaccccatc gaccttgccg 1400  
 ccctgcactg ctgccagagg ctgaaggaag agcagtggga ggtggaggac 1450  
 ttgatgaggg aattctactc tctcaaacgg agcaggtcga aatttcagaa 1500  
 aaacactggt agttcggggc catgggaacc tccagcaagg ccaggaacac 1550  
 tcttctcacc agaaaaccat gaccaggcaa gggagaggaa gcctgccaaa 1600  
 cagaaggtcc cacttctcag ctgccccagt cagcccttca cctccaagtt 1650  
 ggcattactg ggacagggtt tcttagactc ctcataacca ctggataatt 1700  
 tttttatatt tatttttttg aggctaaact ataataaatt gcttttggct 1750  
 atcataaaa 1759

<210> 181  
 <211> 541  
 <212> PRT  
 <213> Homo sapiens

<400> 181  
 Met Pro Phe Arg Leu Leu Ile Pro Leu Gly Leu Leu Cys Ala Leu  
 1 5 10 15  
 Leu Pro Gln His His Gly Ala Pro Gly Pro Asp Gly Ser Ala Pro  
 20 25 30  
 Asp Pro Ala His Tyr Ser Phe Ser Leu Thr Leu Ile Asp Ala Leu  
 35 40 45  
 Asp Thr Leu Leu Ile Leu Gly Asn Val Ser Glu Phe Gln Arg Val  
 50 55 60  
 Val Glu Val Leu Gln Asp Ser Val Asp Phe Asp Ile Asp Val Asn  
 65 70 75  
 Ala Ser Val Phe Glu Thr Asn Ile Arg Val Val Gly Gly Leu Leu  
 80 85 90  
 Ser Ala His Leu Leu Ser Lys Lys Ala Gly Val Glu Val Glu Ala  
 95 100 105  
 Gly Trp Pro Cys Ser Gly Pro Leu Leu Arg Met Ala Glu Glu Ala  
 110 115 120  
 Ala Arg Lys Leu Leu Pro Ala Phe Gln Thr Pro Thr Gly Met Pro

				125						130					135
Tyr	Gly	Thr	Val	Asn	Leu	Leu	His	Gly	Val	Asn	Pro	Gly	Glu	Thr	
				140					145					150	
Pro	Val	Thr	Cys	Thr	Ala	Gly	Ile	Gly	Thr	Phe	Ile	Val	Glu	Phe	
				155					160					165	
Ala	Thr	Leu	Ser	Ser	Leu	Thr	Gly	Asp	Pro	Val	Phe	Glu	Asp	Val	
				170					175					180	
Ala	Arg	Val	Ala	Leu	Met	Arg	Leu	Trp	Glu	Ser	Arg	Ser	Asp	Ile	
				185					190					195	
Gly	Leu	Val	Gly	Asn	His	Ile	Asp	Val	Leu	Thr	Gly	Lys	Trp	Val	
				200					205					210	
Ala	Gln	Asp	Ala	Gly	Ile	Gly	Ala	Gly	Val	Asp	Ser	Tyr	Phe	Glu	
				215					220					225	
Tyr	Leu	Val	Lys	Gly	Ala	Ile	Leu	Leu	Gln	Asp	Lys	Lys	Leu	Met	
				230					235					240	
Ala	Met	Phe	Leu	Glu	Tyr	Asn	Lys	Ala	Ile	Arg	Asn	Tyr	Thr	Arg	
				245					250					255	
Phe	Asp	Asp	Trp	Tyr	Leu	Trp	Val	Gln	Met	Tyr	Lys	Gly	Thr	Val	
				260					265					270	
Ser	Met	Pro	Val	Phe	Gln	Ser	Leu	Glu	Ala	Tyr	Trp	Pro	Gly	Leu	
				275					280					285	
Gln	Ser	Leu	Ile	Gly	Asp	Ile	Asp	Asn	Ala	Met	Arg	Thr	Phe	Leu	
				290					295					300	
Asn	Tyr	Tyr	Thr	Val	Trp	Lys	Gln	Phe	Gly	Gly	Leu	Pro	Glu	Phe	
				305					310					315	
Tyr	Asn	Ile	Pro	Gln	Gly	Tyr	Thr	Val	Glu	Lys	Arg	Glu	Gly	Tyr	
				320					325					330	
Pro	Leu	Arg	Pro	Glu	Leu	Ile	Glu	Ser	Ala	Met	Tyr	Leu	Tyr	Arg	
				335					340					345	
Ala	Thr	Gly	Asp	Pro	Thr	Leu	Leu	Glu	Leu	Gly	Arg	Asp	Ala	Val	
				350					355					360	
Glu	Ser	Ile	Glu	Lys	Ile	Ser	Lys	Val	Glu	Cys	Gly	Phe	Ala	Thr	
				365					370					375	
Ile	Lys	Asp	Leu	Arg	Asp	His	Lys	Leu	Asp	Asn	Arg	Met	Glu	Ser	
				380					385					390	
Phe	Phe	Leu	Ala	Glu	Thr	Val	Lys	Tyr	Leu	Tyr	Leu	Leu	Phe	Asp	
				395					400					405	
Pro	Thr	Asn	Phe	Ile	His	Asn	Asn	Gly	Ser	Thr	Phe	Asp	Ala	Val	
				410					415					420	
Ile	Thr	Pro	Tyr	Gly	Glu	Cys	Ile	Leu	Gly	Ala	Gly	Gly	Tyr	Ile	
				425					430					435	
Phe	Asn	Thr	Glu	Ala	His	Pro	Ile	Asp	Leu	Ala	Ala	Leu	His	Cys	

	440		445		450									
Cys	Gln	Arg	Leu	Lys	Glu	Glu	Gln	Trp	Glu	Val	Glu	Asp	Leu	Met
				455					460					465
Arg	Glu	Phe	Tyr	Ser	Leu	Lys	Arg	Ser	Arg	Ser	Lys	Phe	Gln	Lys
				470					475					480
Asn	Thr	Val	Ser	Ser	Gly	Pro	Trp	Glu	Pro	Pro	Ala	Arg	Pro	Gly
				485					490					495
Thr	Leu	Phe	Ser	Pro	Glu	Asn	His	Asp	Gln	Ala	Arg	Glu	Arg	Lys
				500					505					510
Pro	Ala	Lys	Gln	Lys	Val	Pro	Leu	Leu	Ser	Cys	Pro	Ser	Gln	Pro
				515					520					525
Phe	Thr	Ser	Lys	Leu	Ala	Leu	Leu	Gly	Gln	Val	Phe	Leu	Asp	Ser
				530					535					540

Ser

<210> 182  
 <211> 2056  
 <212> DNA  
 <213> Homo sapiens

<400> 182  
 aaagttacat tttctctgga actctcctag gccactccct gctgatgcaa 50  
 catctggggtt tgggcagaaa ggagggtgct tcggagcccg ccctttctga 100  
 gcttcctggg cgggctctag aacaattcag gcttcgctgc gactcagacc 150  
 tcagctocaa catatgcatt ctgaagaaag atggctgaga tggacagaat 200  
 gctttatttt ggaaagaaac aatgttctag gtcaaactga gtctaccaa 250  
 tgcagacttt cacaatggtt ctagaagaaa tctggacaag tcttttcatg 300  
 tggtttttct acgcattgat tccatgtttg ctcacagatg aagtggccat 350  
 tctgcoctgcc cctcagaacc tctctgtact ctcaaccaac atgaagcatc 400  
 tcttgatgtg gagcccagtg atcgcgctg gagaaacagt gtactattct 450  
 gtogaatacc agggggagta cgagagcctg tacacgagcc acatctggat 500  
 cccagcagc tgggtgtcac tcaactgaagg tcctgagtgt gatgtcactg 550  
 atgacatcac ggccactgtg ccatacaacc ttcgtgtcag ggccacattg 600  
 ggctcacaga cctcagcctg gagcatcctg aagcatccct ttaatagaaa 650  
 ctcaaccatc cttacccgac ctgggatgga gatcaccaaa gatggcttcc 700  
 acctgggttat tgagctggag gacctggggc cccagtttga gttccttgtg 750  
 gctactgga ggaggagcc tgggtgccgag gaacatgtca aaatggtgag 800  
 gagtgggggt attccagtgc acctagaaac catggagcca ggggctgcat 850

actgtgtgaa ggcccagaca ttcgtgaagg ccattgggag gtacagcgcc 900  
 ttcagccaga cagaatgtgt ggaggtgcaa ggagaggcca ttcccctggt 950  
 actggccctg tttgcctttg ttggcttcat gctgatcctt gtggtcgtgc 1000  
 cactgttcgt ctggaaaatg ggccggctgc tccagtactc ctgttgcccc 1050  
 gtggtggtcc tcccagacac cttgaaaata accaattcac cccagaagtt 1100  
 aatcagctgc agaagggagg aggtggatgc ctgtgccacg gctgtgatgt 1150  
 ctcttgagga actcctcagg gcctggatct cataggtttg cggaagggcc 1200  
 caggtgaagc cgagaacctg gtctgcatga catggaaacc atgaggggac 1250  
 aagttgtgtt tctgttttcc gccacggaca agggatgaga gaagtaggaa 1300  
 gagcctgttg tctacaagtc tagaagcaac catcagaggc agggtggttt 1350  
 gtctaacaga aactgactg aggccttaggg gatgtgacct ctagactggg 1400  
 ggctgccact tgctggctga gcaaccctgg gaaaagtgac ttcacccctt 1450  
 cggtcctaag tttttctcct tgtaatgggg gaattaccta cacacctgct 1500  
 aaacacacac acacagagtc tctctctata tatacacacg tacacataaa 1550  
 tacaccacgc acttgcaagg ctagagggaa actggtgaca ctctacagtc 1600  
 tgactgattc agtgtttctg gagagcagga cataaatgta tgatgagaat 1650  
 gatcaaggac tctacacact ggggtggcttg gagagcccac tttcccagaa 1700  
 taatccttga gagaaaagga atcatgggag caatggtgtt gagttcactt 1750  
 caagcccaat gccggtgcag aggggaatgg cttagcgagc tctacagtag 1800  
 gtgaacctga ggaaggtcac agccacactg aaaatgggat gtgcatgaac 1850  
 acggaggatc catgaactac tgtaaagtgt tgacagtgtg tgcacactgc 1900  
 agacagcagg tgaaatgtat gtgtgcaatg cgacgagaat gcagaagtca 1950  
 gtaacatgtg catgtttgtt gtgctccttt tttctgttgg taaagtacag 2000  
 aattcagcaa ataaaaaggg ccaccctggc caaaagcggg aaaaaaaaaa 2050  
 aaaaaa 2056

- <210> 183
- <211> 311
- <212> PRT
- <213> Homo sapiens
- <220>
- <221> Signal peptide
- <222> 1-29
- <223> Signal peptide
- <220>
- <221> N-glycosylation sites
- <222> 40-43, 134-137

<223> N-glycosylation sites.

<220>

<221> Tissue factor proteins homology

<222> 92-119

<223> Tissue factor proteins homology

<220>

<221> Transmembrane domain

<222> 230-255

<223> Transmembrane domain

<220>

<221> Integrins alpha chain protein homology

<222> 232-262

<223> Integrins alpha chain protein homology

<400> 183

Met	Gln	Thr	Phe	Thr	Met	Val	Leu	Glu	Glu	Ile	Trp	Thr	Ser	Leu	
1				5					10					15	
Phe	Met	Trp	Phe	Phe	Tyr	Ala	Leu	Ile	Pro	Cys	Leu	Leu	Thr	Asp	
				20					25					30	
Glu	Val	Ala	Ile	Leu	Pro	Ala	Pro	Gln	Asn	Leu	Ser	Val	Leu	Ser	
				35					40					45	
Thr	Asn	Met	Lys	His	Leu	Leu	Met	Trp	Ser	Pro	Val	Ile	Ala	Pro	
				50					55					60	
Gly	Glu	Thr	Val	Tyr	Tyr	Ser	Val	Glu	Tyr	Gln	Gly	Glu	Tyr	Glu	
				65					70					75	
Ser	Leu	Tyr	Thr	Ser	His	Ile	Trp	Ile	Pro	Ser	Ser	Trp	Cys	Ser	
				80					85					90	
Leu	Thr	Glu	Gly	Pro	Glu	Cys	Asp	Val	Thr	Asp	Asp	Ile	Thr	Ala	
				95					100					105	
Thr	Val	Pro	Tyr	Asn	Leu	Arg	Val	Arg	Ala	Thr	Leu	Gly	Ser	Gln	
				110					115					120	
Thr	Ser	Ala	Trp	Ser	Ile	Leu	Lys	His	Pro	Phe	Asn	Arg	Asn	Ser	
				125					130					135	
Thr	Ile	Leu	Thr	Arg	Pro	Gly	Met	Glu	Ile	Thr	Lys	Asp	Gly	Phe	
				140					145					150	
His	Leu	Val	Ile	Glu	Leu	Glu	Asp	Leu	Gly	Pro	Gln	Phe	Glu	Phe	
				155					160					165	
Leu	Val	Ala	Tyr	Trp	Arg	Arg	Glu	Pro	Gly	Ala	Glu	Glu	His	Val	
				170					175					180	
Lys	Met	Val	Arg	Ser	Gly	Gly	Ile	Pro	Val	His	Leu	Glu	Thr	Met	
				185					190					195	
Glu	Pro	Gly	Ala	Ala	Tyr	Cys	Val	Lys	Ala	Gln	Thr	Phe	Val	Lys	
				200					205					210	
Ala	Ile	Gly	Arg	Tyr	Ser	Ala	Phe	Ser	Gln	Thr	Glu	Cys	Val	Glu	
				215					220					225	



Val	Gln	Gly	Glu	Ala	Ile	Pro	Leu	Val	Leu	Ala	Leu	Phe	Ala	Phe	
				230					235					240	
Val	Gly	Phe	Met	Leu	Ile	Leu	Val	Val	Val	Pro	Leu	Phe	Val	Trp	
				245					250					255	
Lys	Met	Gly	Arg	Leu	Leu	Gln	Tyr	Ser	Cys	Cys	Pro	Val	Val	Val	
				260					265					270	
Leu	Pro	Asp	Thr	Leu	Lys	Ile	Thr	Asn	Ser	Pro	Gln	Lys	Leu	Ile	
				275					280					285	
Ser	Cys	Arg	Arg	Glu	Glu	Val	Asp	Ala	Cys	Ala	Thr	Ala	Val	Met	
				290					295					300	
Ser	Pro	Glu	Glu	Leu	Leu	Arg	Ala	Trp	Ile	Ser					
				305					310						

<210> 184  
 <211> 808  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 654, 711, 748  
 <223> unknown base

<400> 184  
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 cctttctagc ttcttgccg gctctagaac aattcaggct tcgctgcgac 100  
 tagacctcag ctccaacata tgcattctga agaaagatgg ctgagatgac 150  
 agaatgcttt attttgaaa gaaacaatgt tctaggtcaa actgagtcta 200  
 ccaaatgcag actttcacia tggttctaga agaaatctgg acaagtcttt 250  
 tcatgtggtt tttctacgca ttgattccat gtttgtcac agatgaagtg 300  
 gccattctgc ctgcccctca gaacctctct gtactctcaa ccaacatgaa 350  
 gcatctcttg atgtggagcc cagtgatcgc gcctggagaa acagtgtact 400  
 attctgtcga ataccagggg gactacgaga gcctgtacac gagccacatc 450  
 tggatcccca gcagctggtg ctactcaact gaaggtcctg agtgtgatgt 500  
 cactgatgac atcacggcca ctgtgccata caacctttgt gtcagggcca 550  
 cattgggctc acagacctca gcctggagca tctgaagca tccctttaat 600  
 agaaactcaa ccaccttac ccgacctggg atggagatca ccaaagatgg 650  
 cttncacctg gttattgagc tggaggacct ggggccccag tttgagttcc 700  
 ttgtggccta ntggaggagg ggcgaacccc ttgcggcgca aggggttngc 750  
 gaacccttg cggccgctgg ggtatctctc gagaaaagag aggcccaata 800  
 tgaccac 808

<210> 185  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 185  
aggcttcgct gcgactagac ctc 23

<210> 186  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 186  
ccaggtcggg taaggatggt tgag 24

<210> 187  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 187  
tttctacgca ttgattccat gtttgctcac agatgaagtg gccattctgc 50

<210> 188  
<211> 1227  
<212> DNA  
<213> Homo sapiens

<400> 188  
cggacgcgtg ggccgccacc tccggaacaa gccatggtgg cggcgacggt 50  
ggcagcggcg tggctgctcc tgtgggctgc ggcctgcgcg cagcaggagc 100  
aggacttcta cgacttcaag gcggtcaaca tccggggcaa actggtgtcg 150  
ctggagaagt accgcggatc ggtgtccctg gtggtgaatg tggccagcga 200  
gtgcggcttc acagaccagc actaccgagc cctgcagcag ctgcagcgag 250  
acctgggccc ccaccacttt aacgtgctcg ccttcccctg caaccagttt 300  
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<210> 189  
 <211> 187  
 <212> PRT  
 <213> Homo sapiens

<400> 189  
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                     20                    25                    30  
 Val Asn Ile Arg Gly Lys Leu Val Ser Leu Glu Lys Tyr Arg Gly  
                     35                    40                    45  
 Ser Val Ser Leu Val Val Asn Val Ala Ser Glu Cys Gly Phe Thr  
                     50                    55                    60  
 Asp Gln His Tyr Arg Ala Leu Gln Gln Leu Gln Arg Asp Leu Gly  
                     65                    70                    75  
 Pro His His Phe Asn Val Leu Ala Phe Pro Cys Asn Gln Phe Gly  
                     80                    85                    90  
 Gln Gln Glu Pro Asp Ser Asn Lys Glu Ile Glu Ser Phe Ala Arg  
                     95                    100                    105  
 Arg Thr Tyr Ser Val Ser Phe Pro Met Phe Ser Lys Ile Ala Val  
                     110                    115                    120  
 Thr Gly Thr Gly Ala His Pro Ala Phe Lys Tyr Leu Ala Gln Thr  
                     125                    130                    135  
 Ser Gly Lys Glu Pro Thr Trp Asn Phe Trp Lys Tyr Leu Val Ala  
                     140                    145                    150  
 Pro Asp Gly Lys Val Val Gly Ala Trp Asp Pro Thr Val Ser Val

	155	160	165
Glu Glu Val Arg	Pro Gln Ile Thr Ala Leu Val Arg Lys Leu Ile		
	170	175	180
Leu Leu Lys Arg	Glu Asp Leu		
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<210> 190  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 190  
 gcaggacttc tacgacttca aggc 24

<210> 191  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 191  
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<210> 192  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 192  
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<210> 193  
 <211> 2187  
 <212> DNA  
 <213> Homo sapiens

<400> 193  
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 ctggggggccc gggccgcctt ctctcggagt tggcaggaag ccaggttgca 150  
 ggggtgtccgc ttcctcagtt ccagagaggt ggatcgcgat gtctccacgc 200  
 ccatcggagg cctcagctac gttcaggggt gcacaaaaa gcatcttaac 250  
 agcaagactg tgggocagtg cctggagacc acagcacaga ggggtcccaga 300  
 acgagaggcc ttggtcgtcc tccatgaaga cgtcagggtg acctttgccc 350  
 aactcaagga ggaggtggac aaagctgctt ctggcctcct gagcattggc 400

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 agtgcagggt gtgggagtga aggacgatcg gatgggggaa gagatttgtg 1700  
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 aacttcgaga gcagatggaa cgacatctaa atctgtgaat aaagcagcag 1900  
 gcctgtcctg gccggttggc ttgactctct cctgtcagaa tgcaacctgg 1950  
 ctttatgcac ctagatgtcc ccagcaccca gttctgagcc aggcacatca 2000

aatgtcaagg aattgactga acgaactaag agctcctgga tgggtccggg 2050  
aactcgcctg ggcacaaggt gccaaaaggc aggcagcctg cccaggccct 2100  
ccctcctgtc catccccccac attcccctgt ctgtccttgt gatttggcat 2150  
aaagagcttc tgttttcttt gaaaaaaaaa aaaaaaa 2187

<210> 194  
<211> 615  
<212> PRT  
<213> Homo sapiens

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35 40 45  
Glu Val Asp Arg Met Val Ser Thr Pro Ile Gly Gly Leu Ser Tyr  
50 55 60  
Val Gln Gly Cys Thr Lys Lys His Leu Asn Ser Lys Thr Val Gly  
65 70 75  
Gln Cys Leu Glu Thr Thr Ala Gln Arg Val Pro Glu Arg Glu Ala  
80 85 90  
Leu Val Val Leu His Glu Asp Val Arg Leu Thr Phe Ala Gln Leu  
95 100 105  
Lys Glu Glu Val Asp Lys Ala Ala Ser Gly Leu Leu Ser Ile Gly  
110 115 120  
Leu Cys Lys Gly Asp Arg Leu Gly Met Trp Gly Pro Asn Ser Tyr  
125 130 135  
Ala Trp Val Leu Met Gln Leu Ala Thr Ala Gln Ala Gly Ile Ile  
140 145 150  
Leu Val Ser Val Asn Pro Ala Tyr Gln Ala Met Glu Leu Glu Tyr  
155 160 165  
Val Leu Lys Lys Val Gly Cys Lys Ala Leu Val Phe Pro Lys Gln  
170 175 180  
Phe Lys Thr Gln Gln Tyr Tyr Asn Val Leu Lys Gln Ile Cys Pro  
185 190 195  
Glu Val Glu Asn Ala Gln Pro Gly Ala Leu Lys Ser Gln Arg Leu  
200 205 210  
Pro Asp Leu Thr Thr Val Ile Ser Val Asp Ala Pro Leu Pro Gly  
215 220 225  
Thr Leu Leu Leu Asp Glu Val Val Ala Ala Gly Ser Thr Arg Gln  
230 235 240  
His Leu Asp Gln Leu Gln Tyr Asn Gln Gln Phe Leu Ser Cys His

	245		250		255
Asp Pro Ile Asn	Ile Gln Phe Thr Ser	Gly Thr Thr Gly Ser	Pro		
	260		265		270
Lys Gly Ala Thr	Leu Ser His Tyr Asn	Ile Val Asn Asn Ser	Asn		
	275		280		285
Ile Leu Gly Glu	Arg Leu Lys Leu His	Glu Lys Thr Pro Glu	Gln		
	290		295		300
Leu Arg Met Ile	Leu Pro Asn Pro Leu	Tyr His Cys Leu Gly	Ser		
	305		310		315
Val Ala Gly Thr	Met Met Cys Leu Met	Tyr Gly Ala Thr Leu	Ile		
	320		325		330
Leu Ala Ser Pro	Ile Phe Asn Gly Lys	Lys Ala Leu Glu Ala	Ile		
	335		340		345
Ser Arg Glu Arg	Gly Thr Phe Leu Tyr	Gly Thr Pro Thr Met	Phe		
	350		355		360
Val Asp Ile Leu	Asn Gln Pro Asp Phe	Ser Ser Tyr Asp Ile	Ser		
	365		370		375
Thr Met Cys Gly	Gly Val Ile Ala Gly	Ser Pro Ala Pro Pro	Glu		
	380		385		390
Leu Ile Arg Ala	Ile Ile Asn Lys Ile	Asn Met Lys Asp Leu	Val		
	395		400		405
Val Ala Tyr Gly	Thr Thr Glu Asn Ser	Pro Val Thr Phe Ala	His		
	410		415		420
Phe Pro Glu Asp	Thr Val Glu Gln Lys	Ala Glu Ser Val Gly	Arg		
	425		430		435
Ile Met Pro His	Thr Glu Ala Arg Ile	Met Asn Met Glu Ala	Gly		
	440		445		450
Thr Leu Ala Lys	Leu Asn Thr Pro Gly	Glu Leu Cys Ile Arg	Gly		
	455		460		465
Tyr Cys Val Met	Leu Gly Tyr Trp Gly	Glu Pro Gln Lys Thr	Glu		
	470		475		480
Glu Ala Val Asp	Gln Asp Lys Trp Tyr	Trp Thr Gly Asp Val	Ala		
	485		490		495
Thr Met Asn Glu	Gln Gly Phe Cys Lys	Ile Val Gly Arg Ser	Lys		
	500		505		510
Asp Met Ile Ile	Arg Gly Gly Glu Asn	Ile Tyr Pro Ala Glu	Leu		
	515		520		525
Glu Asp Phe Phe	His Thr His Pro Lys	Val Gln Glu Val Gln	Val		
	530		535		540
Val Gly Val Lys	Asp Asp Arg Met Gly	Glu Glu Ile Cys Ala	Cys		
	545		550		555
Ile Arg Leu Lys	Asp Gly Glu Glu Thr	Thr Val Glu Glu Ile	Lys		

					560						565						570
Ala	Phe	Cys	Lys	Gly	Lys	Ile	Ser	His	Phe	Lys	Ile	Pro	Lys	Tyr			
				575					580					585			
Ile	Val	Phe	Val	Thr	Asn	Tyr	Pro	Leu	Thr	Ile	Ser	Gly	Lys	Ile			
				590					595					600			
Gln	Lys	Phe	Lys	Leu	Arg	Glu	Gln	Met	Glu	Arg	His	Leu	Asn	Leu			
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<210> 195
<211> 642
<212> DNA
<213> Homo sapiens
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<210> 196
<211> 1575
<212> DNA
<213> Homo sapiens
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 ctgagccggg aggcgtgccg gggtagatcg ccgccgggtc tgagctgcta 500  
 caacgccagc gatcatgtct acaagggctg cttcgacggc aacgtcacct 550  
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 gatgaattct gcaactcggga tggagtaaca ggcccagggt tcacgctcag 650  
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 gccagcccc tgtttttcca acattcccca gtatccccag cttctgctgc 1200  
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 ggggtgttcta gctttttgag gacagctcct gtatccttct catccttgtc 1300  
 totccgcttg tctctttgtg atgttaggac agagtgagag aagtcagctg 1350  
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 tagccagcct ggactttgga gcgtggggtg ggtgggacaa tggctcccca 1450  
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<210> 197

<211> 346

<212> PRT

<213> Homo sapiens

<400> 197

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Ala	Gly	Trp	Leu	Leu	Leu	Leu	Leu	Leu	Arg	Gly	Gly	Ala	Gln	Ala
			20						25					30

Leu Glu Cys Tyr Ser Cys Val Gln Lys Ala Asp Asp Gly Cys Ser

10346650

	35	40	45
Pro Asn Lys Met Lys Thr Val Lys Cys Ala	50	55	60
Cys Thr Glu Ala Val Gly Ala Val Glu Thr	65	70	75
Ser Leu Ala Val Arg Gly Cys Gly Ser Gly	80	85	90
Asp Arg Gly Leu Asp Leu His Gly Leu Leu	95	100	105
Gln Gln Cys Ala Gln Asp Arg Cys Asn Ala	110	115	120
Ser Arg Ala Leu Asp Pro Ala Gly Asn Glu	125	130	135
Asn Gly Val Glu Cys Tyr Ser Cys Val Gly	140	145	150
Cys Gln Gly Thr Ser Pro Pro Val Val Ser	155	160	165
Asp His Val Tyr Lys Gly Cys Phe Asp Gly	170	175	180
Ala Ala Asn Val Thr Val Ser Leu Pro Val	185	190	195
Asp Glu Phe Cys Thr Arg Asp Gly Val Thr	200	205	210
Leu Ser Gly Ser Cys Cys Gln Gly Ser Arg	215	220	225
Arg Asn Lys Thr Tyr Phe Ser Pro Arg Ile	230	235	240
Leu Pro Pro Pro Glu Pro Thr Thr Val Ala	245	250	255
Thr Thr Ser Thr Ser Ala Pro Val Arg Pro	260	265	270
Pro Met Pro Ala Pro Thr Ser Gln Thr Pro	275	280	285
His Glu Ala Ser Arg Asp Glu Glu Pro Arg	290	295	300
Ala Gly His Gln Asp Arg Ser Asn Ser Gly	305	310	315
Gly Gly Pro Gln Gln Pro His Asn Lys Gly	320	325	330
Ala Gly Leu Ala Ala Leu Leu Leu Ala Val	335	340	345

Leu

<210> 198  
 <211> 1657  
 <212> DNA  
 <213> Homo sapiens

<400> 198  
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 gtcctggcca gtgcagctga aaaggagaag gaaatggacc cttttcatta 150  
 tgattaccag accctgagga ttgggggact ggtgttcgct gtggtcctct 200  
 tctcggttgg gatcctcctt atcctaagtc gcaggtgcaa gtgcagtttc 250  
 aatcagaagc cccgggcccc aggagatgag gaagcccagg tggagaacct 300  
 catcacggcc aatgcaacag agccccagaa gcagagaact gaagtgcagc 350  
 catcaggtgg aagcctctgg aacctgaggc ggctgcttga acctttggat 400  
 gcaaattgtc atgcttaaga aaaccggcca cttcagcaac agccctttcc 450  
 ccaggagaag ccaagaactt gtgtgtcccc caccctatcc cctctaacac 500  
 cattcctcca cctgatgatg caactaacac ttgcctcccc actgcagcct 550  
 gcggtcctgc ccacctcccg tgatgtgtgt gtgtgtgtgt gtgtgtgact 600  
 gtgtgtgttt gctaactgtg gtctttgtgg ctacttgttt gtggatggta 650  
 ttgtgtttgt tagtgaactg tggactcgct ttcccaggca ggggctgagc 700  
 cacatggcca tctgctcctc cctgcccccg tggccctcca tcaccttctg 750  
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 cagtccctgc aattgggtct ctggcaggca atagttgaag gactcctggt 1300  
 ccgttggggc cagcacaccg ggatggatgg agggagagca gaggcctttg 1350  
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cattttccat ccaaa 415

<210> 201

<211> 99

<212> PRT

<213> Homo sapiens

<400> 201

Met Lys Ile Pro Val Leu Pro Ala Val Val Leu Leu Ser Leu Leu  
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Val Leu His Ser Ala Gln Gly Ala Thr Leu Gly Gly Pro Glu Glu  
20 25 30

Glu Ser Thr Ile Glu Asn Tyr Ala Ser Arg Pro Glu Ala Phe Asn  
35 40 45

Thr Pro Phe Leu Asn Ile Asp Lys Leu Arg Ser Ala Phe Lys Ala  
50 55 60

Asp Glu Phe Leu Asn Trp His Ala Leu Phe Glu Ser Ile Lys Arg  
65 70 75

Lys Leu Pro Phe Leu Asn Trp Asp Ala Phe Pro Lys Leu Lys Gly  
80 85 90

Leu Arg Ser Ala Thr Pro Asp Ala Gln  
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<210> 202

<211> 678

<212> DNA

<213> Homo sapiens

<400> 202

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cagcaggagt ctcccagggt gttcttctcc agccagttcc aactcaggag 150

acagggtccca aggccatggg agatctctcc tgtggctttg ccggccaactc 200

atgagagtgt ttttgtgtaa agtatttttt agaatactgt tgacttcttc 250

atgatttaat aaccatcctt tgcgaagttt tatgaggctt taggggaatg 300

tcaaccctca aatttttggt atactagatg gcttccattt acccaccact 350

attttaagggt ccctttatctt ttaggttcaa gggtcatctg acttgagaaa 400

gtgcccttct gcagcttcat tgattttggt tatcttcact attaattgta 450

acgattaataa aagaataaga gcacgcagac ctctaggaga atattttatc 500

cctgggtgcc cctgacacat ttatgtagtg atcccacaaa tgtgattggt 550

aatttaaagt ttattctaatt attagtacat tcagttgtga tgtaatatga 600

ataaccagaa tctatttctt aaaagttttg agtatatttt tcaactagat 650

atttgtatag aaagactgaa tagtgatg 678

<210> 203  
 <211> 52  
 <212> PRT  
 <213> Homo sapiens

<400> 203  
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 1 5 10 15  
 Ser Leu Leu Ala Ala Gly Val Ser Gln Val Val Leu Leu Gln Pro  
 20 25 30  
 Val Pro Thr Gln Glu Thr Gly Pro Lys Ala Met Gly Asp Leu Ser  
 35 40 45  
 Cys Gly Phe Ala Gly His Ser  
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<210> 204  
 <211> 1917  
 <212> DNA  
 <213> Homo sapiens

<400> 204  
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 agaaggagtc aggttcaaaa tggaaagtat ttattgacca aattaacagg 150  
 tctttggaga attacgaacc atgttcaagt caaaactgca gctgctacca 200  
 tgggtgcata gaagaggatc taactccttt ccgaggaggc atctccagga 250  
 agatgatggc agaggtagtc agacggaagc tagggacca ctatcagatc 300  
 actaagaaca gactgtaccg ggaaaatgac tgcattgtcc cctcaagggtg 350  
 tagtgggtgt gagcaactta ttttggaagt gatcgggcgt ctccctgaca 400  
 tggagatggg gatcaatgta cgagattatc ctgaggttcc taaatggatg 450  
 gagcctgcc tccagtcctt ctcttcagc aagacatcag agtaccatga 500  
 tatcatgtat cctgcttggc ctttttggga agggggacct gctgtttggc 550  
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cgagaaggaa aggttatgat caaattattc ccaaaatgtt gaaaactgaa 1200  
ctatagtagt catcatagga ccatagtcct ctttgtggca acagatctca 1250  
gatatcctac ggtgagaagc ttaccataag cttggctcct ataccttgaa 1300  
tatctgctat caagccaaat acctggtttt ccttatcatg ctgcacccag 1350  
agcaactcct gagaaagatt taaaatgtgt ctaatacact gatatgaagc 1400  
agttcaactt tttggatgaa taaggaccag aaatcgtgag atgtggattt 1450  
tgaacccaac tctaccttc attttcttaa gaccaatcac agcttgtgcc 1500  
tcagatcatc cacctgtgtg agtccatcac tgtgaaattg actgtgtcca 1550  
tgtgatgatg ccttttgtcc cattatttgg agcagaaaat tcgtcatttg 1600  
gaagtagtac aactcattgc tggaattgtg aaattattca aggcgtgatc 1650  
tctgtcactt tattttaatg taggaaaccc tatgggggtt atgaaaaata 1700  
cttggggatc attctctgaa tggcttaagg aagcggtagc catgccatgc 1750  
aatgatgtag gagttctctt ttgtaaaacc ataaactctg ttactcagga 1800  
ggtttctata atgccacata gaaagaggcc aattgcatga gtaattattg 1850  
caattggatt tcaggttccc tttttgtgcc ttcatgccct acttcttaat 1900  
gcctctctaa agccaaa 1917

<210> 205  
<211> 392  
<212> PRT  
<213> Homo sapiens

<400> 205  
Met Glu Trp Trp Ala Ser Ser Pro Leu Arg Leu Trp Leu Leu Leu  
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Phe Leu Leu Pro Ser Ala Gln Gly Arg Gln Lys Glu Ser Gly Ser  
20 25 30  
Lys Trp Lys Val Phe Ile Asp Gln Ile Asn Arg Ser Leu Glu Asn  
35 40 45  
Tyr Glu Pro Cys Ser Ser Gln Asn Cys Ser Cys Tyr His Gly Val  
50 55 60  
Ile Glu Glu Asp Leu Thr Pro Phe Arg Gly Gly Ile Ser Arg Lys  
65 70 75  
Met Met Ala Glu Val Val Arg Arg Lys Leu Gly Thr His Tyr Gln  
80 85 90  
Ile Thr Lys Asn Arg Leu Tyr Arg Glu Asn Asp Cys Met Phe Pro

															95																100																105
Ser	Arg	Cys	Ser	Gly	Val	Glu	His	Phe	Ile	Leu	Glu	Val	Ile	Gly	110	115	120																														
Arg	Leu	Pro	Asp	Met	Glu	Met	Val	Ile	Asn	Val	Arg	Asp	Tyr	Pro	125	130	135																														
Gln	Val	Pro	Lys	Trp	Met	Glu	Pro	Ala	Ile	Pro	Val	Phe	Ser	Phe	140	145	150																														
Ser	Lys	Thr	Ser	Glu	Tyr	His	Asp	Ile	Met	Tyr	Pro	Ala	Trp	Thr	155	160	165																														
Phe	Trp	Glu	Gly	Gly	Pro	Ala	Val	Trp	Pro	Ile	Tyr	Pro	Thr	Gly	170	175	180																														
Leu	Gly	Arg	Trp	Asp	Leu	Phe	Arg	Glu	Asp	Leu	Val	Arg	Ser	Ala	185	190	195																														
Ala	Gln	Trp	Pro	Trp	Lys	Lys	Lys	Asn	Ser	Thr	Ala	Tyr	Phe	Arg	200	205	210																														
Gly	Ser	Arg	Thr	Ser	Pro	Glu	Arg	Asp	Pro	Leu	Ile	Leu	Leu	Ser	215	220	225																														
Arg	Lys	Asn	Pro	Lys	Leu	Val	Asp	Ala	Glu	Tyr	Thr	Lys	Asn	Gln	230	235	240																														
Ala	Trp	Lys	Ser	Met	Lys	Asp	Thr	Leu	Gly	Lys	Pro	Ala	Ala	Lys	245	250	255																														
Asp	Val	His	Leu	Val	Asp	His	Cys	Lys	Tyr	Lys	Tyr	Leu	Phe	Asn	260	265	270																														
Phe	Arg	Gly	Val	Ala	Ala	Ser	Phe	Arg	Phe	Lys	His	Leu	Phe	Leu	275	280	285																														
Cys	Gly	Ser	Leu	Val	Phe	His	Val	Gly	Asp	Glu	Trp	Leu	Glu	Phe	290	295	300																														
Phe	Tyr	Pro	Gln	Leu	Lys	Pro	Trp	Val	His	Tyr	Ile	Pro	Val	Lys	305	310	315																														
Thr	Asp	Leu	Ser	Asn	Val	Gln	Glu	Leu	Leu	Gln	Phe	Val	Lys	Ala	320	325	330																														
Asn	Asp	Asp	Val	Ala	Gln	Glu	Ile	Ala	Glu	Arg	Gly	Ser	Gln	Phe	335	340	345																														
Ile	Arg	Asn	His	Leu	Gln	Met	Asp	Asp	Ile	Thr	Cys	Tyr	Trp	Glu	350	355	360																														
Asn	Leu	Leu	Ser	Glu	Tyr	Ser	Lys	Phe	Leu	Ser	Tyr	Asn	Val	Thr	365	370	375																														
Arg	Arg	Lys	Gly	Tyr	Asp	Gln	Ile	Ile	Pro	Lys	Met	Leu	Lys	Thr	380	385	390																														
Glu	Leu																																														

<210> 206



<211> 1425  
<212> DNA  
<213> Homo sapiens

<400> 206  
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ccctcgccctc tttcatcctg gcctttggca ccggagtgga gttcgtgcgc 100  
tttacctccc ttccggccact tcttggaggg atcccggagt ctggtggtcc 150  
ggatgcccgc cagggatggc tggctgccct gcaggaccgc agcatccttg 200  
ccccctggc atgggatctg gggctcctgc ttctatttgt tgggcagcac 250  
agcctcatgg cagctgaaag agtgaaggca tggacatccc ggtacttttg 300  
ggtccttcag aggtcactgt atgtggcctg cactgccctg gccttgcac 350  
tggtgatgcg gtactgggag ccataccca aaggccctgt gttgtgggag 400  
gctcgggctg agccatgggc cacctgggtg ccgctcctct gctttgtgct 450  
ccatgtcatc tcctggctcc tcatctttag catccttctc gtctttgact 500  
atgctgagct catgggcctc aaacaggtat actaccatgt gctggggctg 550  
ggcgagcctc tggccctgaa gtctccccgg gctctcagac tcttctccca 600  
cctgcgccac ccagtgtgtg tggagctgct gacagtgcctg tgggtggtgc 650  
ctaccctggg caccgaccgt ctctccttg ctttcctcct taccctctac 700  
ctgggcctgg ctacgggct tgatcagcaa gacctccgt acctccgggc 750  
ccagctacaa agaaaactcc acctgctctc tcggccccag gatggggagg 800  
cagagtgagg agctcactct ggttacaagc cctgttcttc ctctccact 850  
gaattctaaa tccttaacat ccaggccctg gctgcttcat gccagaggcc 900  
caaatccatg gactgaagga gatgccctt ctactacttg agactttatt 950  
ctctgggtcc agctccatac cctaaattct gagtttcagc cactgaactc 1000  
caaggtccac ttctcaccag caaggaagag tggggtatgg aagtcactctg 1050  
tcccttcaact gtttagagca tgacactctc cccctcaaca gcctcctgag 1100  
aaggaaagga tctgccctga ccactccctt ggcactgtta cttgcctctg 1150  
cgctcaggg gtcccttct gcaccgtgg cttccactcc aagaagggtg 1200  
accaggtct gcaagttcaa cggtcatagc tgtccctcca ggccccaacc 1250  
ttgcctcacc actccggcc ctagtctctg cacctcctta ggccctgct 1300  
ctgggctcag accccaacct agtcaagggg attctcctgc tottaactcg 1350  
atgacttggg gctccctgct ctcccgagga agatgctctg caggaaaata 1400  
aaagtcagcc tttttctaaa aaaaa 1425

<210> 207  
 <211> 262  
 <212> PRT  
 <213> Homo sapiens

<400> 207

Met	Ala	Pro	Ala	Leu	Leu	Leu	Ile	Pro	Ala	Ala	Leu	Ala	Ser	Phe	
1				5					10					15	
Ile	Leu	Ala	Phe	Gly	Thr	Gly	Val	Glu	Phe	Val	Arg	Phe	Thr	Ser	
				20					25					30	
Leu	Arg	Pro	Leu	Leu	Gly	Gly	Ile	Pro	Glu	Ser	Gly	Gly	Pro	Asp	
				35					40					45	
Ala	Arg	Gln	Gly	Trp	Leu	Ala	Ala	Leu	Gln	Asp	Arg	Ser	Ile	Leu	
				50					55					60	
Ala	Pro	Leu	Ala	Trp	Asp	Leu	Gly	Leu	Leu	Leu	Leu	Phe	Val	Gly	
				65					70					75	
Gln	His	Ser	Leu	Met	Ala	Ala	Glu	Arg	Val	Lys	Ala	Trp	Thr	Ser	
				80					85					90	
Arg	Tyr	Phe	Gly	Val	Leu	Gln	Arg	Ser	Leu	Tyr	Val	Ala	Cys	Thr	
				95					100					105	
Ala	Leu	Ala	Leu	Gln	Leu	Val	Met	Arg	Tyr	Trp	Glu	Pro	Ile	Pro	
				110					115					120	
Lys	Gly	Pro	Val	Leu	Trp	Glu	Ala	Arg	Ala	Glu	Pro	Trp	Ala	Thr	
				125					130					135	
Trp	Val	Pro	Leu	Leu	Cys	Phe	Val	Leu	His	Val	Ile	Ser	Trp	Leu	
				140					145					150	
Leu	Ile	Phe	Ser	Ile	Leu	Leu	Val	Phe	Asp	Tyr	Ala	Glu	Leu	Met	
				155					160					165	
Gly	Leu	Lys	Gln	Val	Tyr	Tyr	His	Val	Leu	Gly	Leu	Gly	Glu	Pro	
				170					175					180	
Leu	Ala	Leu	Lys	Ser	Pro	Arg	Ala	Leu	Arg	Leu	Phe	Ser	His	Leu	
				185					190					195	
Arg	His	Pro	Val	Cys	Val	Glu	Leu	Leu	Thr	Val	Leu	Trp	Val	Val	
				200					205					210	
Pro	Thr	Leu	Gly	Thr	Asp	Arg	Leu	Leu	Leu	Ala	Phe	Leu	Leu	Thr	
				215					220					225	
Leu	Tyr	Leu	Gly	Leu	Ala	His	Gly	Leu	Asp	Gln	Gln	Asp	Leu	Arg	
				230					235					240	
Tyr	Leu	Arg	Ala	Gln	Leu	Gln	Arg	Lys	Leu	His	Leu	Leu	Ser	Arg	
				245					250					255	
Pro	Gln	Asp	Gly	Glu	Ala	Glu									
				260											

<210> 208  
 <211> 2095  
 <212> DNA

<213> Homo sapiens

<400> 208

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gtagttcaca acagatctga gtgttttaaat taagcatgga atacagaaaa 150  
caacaaaaaa cttaagcttt aatttcatct ggaattccac agttttctta 200  
gtcccttgga cccggttgac ctgttggtc ttcccgctgg ctgctctatc 250  
acgtggtgct ctccgactac tcaccccgag tgtaaagaac cttcggctcg 300  
cgtgcttctg agctgctgtg gatggcctcg gctctctgga ctgtccttcc 350  
gagtaggatg tcaactgagat cctcaaatg gagcctcctg ctgctgtcac 400  
tcctgagttt ctttgtgatg tggtaacctc gccttcccca ctacaatgtg 450  
atagaacgcg tgaactggat gtacttctat gagtatgagc cgatttacag 500  
acaagacttt cacttcacac ttogagagca ttcaaactgc tctcatcaaa 550  
atccatttct ggtcattctg gtgacctccc acccttcaga tgtgaaagcc 600  
aggcaggcca ttagagttac ttggggtgaa aaaaagtctt ggtggggata 650  
tgaggttctt acatttttct tattaggcca agaggctgaa aaggaagaca 700  
aaatgttggc attgtcctta gaggatgaac accttcttta tggtgacata 750  
atccgacaag atttttttaga cacatataat aacctgacct tgaaaacat 800  
tatggcattc aggtgggtaa ctgagttttg cccaatgcc aagtacgtaa 850  
tgaagacaga cactgatgtt ttcacataa ctggcaattt agtgaagtat 900  
cttttaaacc taaaccactc agagaagttt ttcacaggtt atcctctaata 950  
tgataattat tcctatagag gattttacca aaaaacccat atttcttacc 1000  
aggagtatcc tttcaagggtg ttccctccat actgcagtgg gttgggttat 1050  
ataatgtcca gagatttggt gccaaagatc tatgaaatga tgggtcacgt 1100  
aaaacccatc aagtttgaag atgtttatgt cgggatctgt ttgaatttat 1150  
taaaagtga cttcatatt ccagaagaca caaatctttt ctttctatat 1200  
agaatccatt tggatgtctg tcaactgaga cgtgtgattg cagcccatgg 1250  
cttttcttcc aaggagatca tcactttttg gcaggatcatg ctaaggaaca 1300  
ccacatgcca ttattaactt cacattctac aaaaagccta gaaggacagg 1350  
ataccttggtg gaaagtgtta aataaagtag gtactgtgga aaattcatgg 1400  
ggaggtcagt gtgtgggtt acactgaact gaaactcatg aaaaaccag 1450  
actggagact ggagggttac acttgtgatt tattagtcag gcccttcaaa 1500

gatgatatgt ggaggaatta aatataaagg aattggaggt ttttgctaaa 1550  
 gaaattaata ggaccaaaca atttggacat gtcattctgt agactagaat 1600  
 ttcttaaaag ggtgttactg agttataagc tcactaggct gtaaaaacaa 1650  
 aacaatgtag agttttatattt attgaacaat gtagtcactt gaaggttttg 1700  
 tgtatatctt atgtggatta ccaatttaaa aatatatgta gttctgtgtc 1750  
 aaaaaacttc ttactgaag ttatactgaa caaaatttta cctgtttttg 1800  
 gtcatttata aagtacttca agatgttgca gtatttcaca gttattatta 1850  
 tttaaaatta cttcaacttt gtgtttttta atgttttgac gatttcaata 1900  
 caagataaaa aggatagtga atcattcttt acatgcaaac attttccagt 1950  
 tacttaactg atcagtttat tattgataca tcactccatt aatgtaaagt 2000  
 cataggtcat tattgcatat cagtaatctc ttggactttg ttaaataattt 2050  
 tactgtggta atatagagaa gaattaaagc aagaaaatct gaaaa 2095

<210> 209  
 <211> 331  
 <212> PRT  
 <213> Homo sapiens

<400> 209  
 Met Ala Ser Ala Leu Trp Thr Val Leu Pro Ser Arg Met Ser Leu  
 1 5 10 15  
 Arg Ser Leu Lys Trp Ser Leu Leu Leu Leu Ser Leu Leu Ser Phe  
 20 25 30  
 Phe Val Met Trp Tyr Leu Ser Leu Pro His Tyr Asn Val Ile Glu  
 35 40 45  
 Arg Val Asn Trp Met Tyr Phe Tyr Glu Tyr Glu Pro Ile Tyr Arg  
 50 55 60  
 Gln Asp Phe His Phe Thr Leu Arg Glu His Ser Asn Cys Ser His  
 65 70 75  
 Gln Asn Pro Phe Leu Val Ile Leu Val Thr Ser His Pro Ser Asp  
 80 85 90  
 Val Lys Ala Arg Gln Ala Ile Arg Val Thr Trp Gly Glu Lys Lys  
 95 100 105  
 Ser Trp Trp Gly Tyr Glu Val Leu Thr Phe Phe Leu Leu Gly Gln  
 110 115 120  
 Glu Ala Glu Lys Glu Asp Lys Met Leu Ala Leu Ser Leu Glu Asp  
 125 130 135  
 Glu His Leu Leu Tyr Gly Asp Ile Ile Arg Gln Asp Phe Leu Asp  
 140 145 150  
 Thr Tyr Asn Asn Leu Thr Leu Lys Thr Ile Met Ala Phe Arg Trp  
 155 160 165

Val	Thr	Glu	Phe	Cys	Pro	Asn	Ala	Lys	Tyr	Val	Met	Lys	Thr	Asp	
				170					175					180	
Thr	Asp	Val	Phe	Ile	Asn	Thr	Gly	Asn	Leu	Val	Lys	Tyr	Leu	Leu	
				185					190					195	
Asn	Leu	Asn	His	Ser	Glu	Lys	Phe	Phe	Thr	Gly	Tyr	Pro	Leu	Ile	
				200					205					210	
Asp	Asn	Tyr	Ser	Tyr	Arg	Gly	Phe	Tyr	Gln	Lys	Thr	His	Ile	Ser	
				215					220					225	
Tyr	Gln	Glu	Tyr	Pro	Phe	Lys	Val	Phe	Pro	Pro	Tyr	Cys	Ser	Gly	
				230					235					240	
Leu	Gly	Tyr	Ile	Met	Ser	Arg	Asp	Leu	Val	Pro	Arg	Ile	Tyr	Glu	
				245					250					255	
Met	Met	Gly	His	Val	Lys	Pro	Ile	Lys	Phe	Glu	Asp	Val	Tyr	Val	
				260					265					270	
Gly	Ile	Cys	Leu	Asn	Leu	Leu	Lys	Val	Asn	Ile	His	Ile	Pro	Glu	
				275					280					285	
Asp	Thr	Asn	Leu	Phe	Phe	Leu	Tyr	Arg	Ile	His	Leu	Asp	Val	Cys	
				290					295					300	
Gln	Leu	Arg	Arg	Val	Ile	Ala	Ala	His	Gly	Phe	Ser	Ser	Lys	Glu	
				305					310					315	
Ile	Ile	Thr	Phe	Trp	Gln	Val	Met	Leu	Arg	Asn	Thr	Thr	Cys	His	
				320					325					330	

Tyr

<210> 210  
 <211> 745  
 <212> DNA  
 <213> Homo sapiens

<400> 210  
 cctctgtcca ctgcttttcgt gaagacaaga tgaagttcac aattgtcttt 50  
 gctggacttc ttggagtctt tctagctcct gccctagcta actataatat 100  
 caacgtcaat gatgacaaca acaatgctgg aagtgggcag cagtcaagtga 150  
 gtgtcaacaa tgaacacaat gtggccaatg ttgacaataa caacggatgg 200  
 gactcctgga attccatctg ggattatgga aatggctttg ctgcaaccag 250  
 actctttcaa aagaagacat gcattgtgca caaaatgaac aaggaagtca 300  
 tgccctccat tcaatccctt gatgcactgg tcaaggaaaa gaagcttcag 350  
 ggtaagggac caggaggacc acctcccaag ggctgatgt actcagtcaa 400  
 cccaaacaaa gtogatgacc tgagcaagtt cggaacaaac attgcaaaca 450  
 tgtgtcgtgg gattccaaca tacatggctg aggagatgca agaggcaagc 500  
 ctgttttttt actcaggaac gtgctacacg accagtgtac tatggattgt 550

ggacatttcc ttctgtggag acacggtgga gaactaaaca atttttttaa 600  
gccactatgg atttagtcat ctgaatatgc tgtgcagaaa aaatatgggc 650  
tccagtgggtt ttaccatgt cattctgaaa tttttctcta ctagttatgt 700  
ttgatttctt taagtttcaa taaaatcatt tagcattgaa aaaaa 745

<210> 211  
<211> 185  
<212> PRT  
<213> Homo sapiens

<400> 211  
Met Lys Phe Thr Ile Val Phe Ala Gly Leu Leu Gly Val Phe Leu  
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Ala Pro Ala Leu Ala Asn Tyr Asn Ile Asn Val Asn Asp Asp Asn  
20 25 30  
Asn Asn Ala Gly Ser Gly Gln Gln Ser Val Ser Val Asn Asn Glu  
35 40 45  
His Asn Val Ala Asn Val Asp Asn Asn Asn Gly Trp Asp Ser Trp  
50 55 60  
Asn Ser Ile Trp Asp Tyr Gly Asn Gly Phe Ala Ala Thr Arg Leu  
65 70 75  
Phe Gln Lys Lys Thr Cys Ile Val His Lys Met Asn Lys Glu Val  
80 85 90  
Met Pro Ser Ile Gln Ser Leu Asp Ala Leu Val Lys Glu Lys Lys  
95 100 105  
Leu Gln Gly Lys Gly Pro Gly Gly Pro Pro Pro Lys Gly Leu Met  
110 115 120  
Tyr Ser Val Asn Pro Asn Lys Val Asp Asp Leu Ser Lys Phe Gly  
125 130 135  
Lys Asn Ile Ala Asn Met Cys Arg Gly Ile Pro Thr Tyr Met Ala  
140 145 150  
Glu Glu Met Gln Glu Ala Ser Leu Phe Phe Tyr Ser Gly Thr Cys  
155 160 165  
Tyr Thr Thr Ser Val Leu Trp Ile Val Asp Ile Ser Phe Cys Gly  
170 175 180  
Asp Thr Val Glu Asn  
185

<210> 212  
<211> 1706  
<212> DNA  
<213> Homo sapiens

<400> 212  
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tacagaagta tattaacttt ttaggagtaa tttctagttt ggattgtaat 100

atgaaataat ttaaaagggc ttcgctcata tataggaaaa tcgcatatgg 150  
tccatagtatt aaattcttat tgcttactga tttttttgag ttaagagttg 200  
ttatatgcta gaatatgagg atgtgaatat aaataagaga agaaaaaaga 250  
ataaagtaga ttgagttctc aatttttatgt aagcttcaga agaactgggt 300  
tgttttacatg caagcttata gttgaaatat ttttcaggaa ttacatgaat 350  
gacagtcttc gaaccaatgt gtttgttcga tttcaaccag agactatagc 400  
atgtgcttgc atctaccttg cagctagagc acttcagatt ccgttgccaa 450  
ctcgtcccca ttggttttctt ctttttggtta ctacagaaga ggaaatccag 500  
gaaatctgca tagaaacact taggctttat accagaaaaa agccaaacta 550  
tgaattactg gaaaaagaag tagaaaaaag aaaagtagcc ttacaagaag 600  
ccaaattaaa agcaaaggga ttgaatccgg atggaactcc agccctttca 650  
accctgggtg gattttctcc agcctccaag ccatcatcac caagagaagt 700  
aaaagctgaa gagaaatcac caatctccat taatgtgaag acagtcaaaa 750  
aagaacctga ggatagacaa caggcttcca aaagccctta caatggtgta 800  
agaaaagaca gcaagagaag tagaaatagc agaagtgcaa gtcgatcgag 850  
gtcaagaaca cgatcacgtt ctagatcaca tactccaaga agacactata 900  
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tcccgcagtc acagtgaag ccctcgaaga catcataatc atggttctcc 1000  
tcaccttaag gccaaagcata ccagagatga tttaaaaagt tcaaacagac 1050  
atggtcataa aaggaaaaaa tctcgttctc gatctcagag caagtctcgg 1100  
gatcactcag atgcagccaa gaaacacagg catgaaaggg gacatcatag 1150  
ggacaggcgt gaacgatctc gtccttttga gaggtcccat aaaagcaagc 1200  
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cttcctttga gcctgcatca gttcttggtt ttgcctatct acagtgtgat 1300  
gtatggactc aatcaaaaac attaaacgca aactgattag gatttgattt 1350  
cttgaaaccc tctaggtctc tagaactgagg aggacagttt cttttgaaaa 1400  
gaactatggt aatttttttg cacattaaaa tgccctagca gtatctaatt 1450  
aaaaaccatg gtcagggttca attgtacttt attatagttg tgtattgttt 1500  
attgctataa gaactggagc gtgaattctg taaaaatgta tcttattttt 1550  
atacagataa aattgcagac actgttctat ttaagtgggt atttgtttaa 1600  
atgatggtga atactttctt aacactgggt tgtctgcatg tgtaaagatt 1650  
tttacaagga aataaaatac aaatcttggt ttttctaaaa aaaaaaaaaa 1700

[illegible]

<400> 213

Met 1	Asn 2	Asp 3	Ser 4	Leu 5	Arg 6	Thr 7	Asn 8	Val 9	Phe 10	Val 11	Arg 12	Phe 13	Gln 14	Pro 15
Glu	Thr	Ile	Ala	Cys 20	Ala	Cys	Ile	Tyr	Leu 25	Ala	Ala	Arg	Ala	Leu 30
Gln	Ile	Pro	Leu	Pro 35	Thr	Arg	Pro	His	Trp 40	Phe	Leu	Leu	Phe	Gly 45
Thr	Thr	Glu	Glu	Glu 50	Ile	Gln	Glu	Ile	Cys 55	Ile	Glu	Thr	Leu	Arg 60
Leu	Tyr	Thr	Arg	Lys 65	Lys	Pro	Asn	Tyr	Glu 70	Leu	Leu	Glu	Lys	Glu 75
Val	Glu	Lys	Arg	Lys 80	Val	Ala	Leu	Gln	Glu 85	Ala	Lys	Leu	Lys	Ala 90
Lys	Gly	Leu	Asn	Pro 95	Asp	Gly	Thr	Pro	Ala 100	Leu	Ser	Thr	Leu	Gly 105
Gly	Phe	Ser	Pro	Ala 110	Ser	Lys	Pro	Ser	Ser 115	Pro	Arg	Glu	Val	Lys 120
Ala	Glu	Glu	Lys	Ser 125	Pro	Ile	Ser	Ile	Asn 130	Val	Lys	Thr	Val	Lys 135
Lys	Glu	Pro	Glu	Asp 140	Arg	Gln	Gln	Ala	Ser 145	Lys	Ser	Pro	Tyr	Asn 150
Gly	Val	Arg	Lys	Asp 155	Ser	Lys	Arg	Ser	Arg 160	Asn	Ser	Arg	Ser	Ala 165
Ser	Arg	Ser	Arg	Ser 170	Arg	Thr	Arg	Ser	Arg 175	Ser	Arg	Ser	His	Thr 180
Pro	Arg	Arg	His	Tyr 185	Asn	Asn	Arg	Arg	Ser 190	Arg	Ser	Gly	Thr	Tyr 195
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Thr	Arg	Asp	Asp	Leu 230	Lys	Ser	Ser	Asn	Arg 235	His	Gly	His	Lys	Arg 240
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Asp	Ala	Ala	Lys	Lys 260	His	Arg	His	Glu	Arg 265	Gly	His	His	Arg	Asp 270
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&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

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&lt;222&gt; 72-73, 85, 91, 127, 226, 268, 454, 484, 513, 566, 663

&lt;223&gt; unknown base

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&lt;211&gt; 1807

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&lt;400&gt; 215

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191

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Pro Leu Leu Ser	Pro Asp Pro Ser Ser	Ala Ser Ala Ala Pro Ile	
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	425	430	435
Gly Ala Leu Gly	Gly Leu Leu Thr Pro	Leu Phe Leu Arg Gly Val	
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Arg	Arg	Ser	Gln	Asp	Gly	Cys	Pro	Asp	Gly	Cys	Ala	Ser	Leu	Thr	
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Ser	Ala	Glu	Asp	Gly	Gln	Pro	Ala	Ile	Ser	Pro	Val	Asp	Ser	Gly	
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Tyr	Arg	Asp	Gly	Val	Ile	Ala	Arg	Asp	Gly	Arg	Leu	Leu	Pro	Gly	
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Leu	Val	Arg	Lys	Val	Asp	Glu	Pro	Gly	Val	Phe	Ile	Phe	Asn	Val	
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Ser Arg Asp Gly	Arg Ile Lys Thr Gly	455	Asp Ile Leu Leu Asn	460	Val 465
Asp Gly Val Glu	Leu Thr Glu Val Ser	470	Arg Ser Glu Ala Val	475	Ala 480
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Val Lys Glu Tyr	Glu Pro Gln Glu Asp	500	Cys Ser Ser Pro Ala	505	Ala 510
Leu Asp Ser Asn	His Asn Met Ala Pro	515	Pro Ser Asp Trp Ser	520	Pro 525
Ser Trp Val Met	Trp Leu Glu Leu Pro	530	Arg Cys Leu Tyr Asn	535	Cys 540
Lys Asp Ile Val	Leu Arg Arg Asn Thr	545	Ala Gly Ser Leu Gly	550	Phe 555
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Phe Ile Lys Ser	Ile Val Glu Gly Thr	575	Pro Ala Tyr Asn Asp	580	Gly 585
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 Lys Asn Thr Ala Ile Val Asn Ile His Ala Gly Ser Cys Ser Ser  
 50 55 60  
 Thr Thr Ile Phe Asp Tyr Lys His Gly Tyr Ile Ala Ser Arg Val  
 65 70 75  
 Leu Ser Arg Arg Ala Cys Phe Ile Leu Lys Met Asp His Gln Asn  
 80 85 90

Ile Pro Pro Leu Asn Asn Leu Gln Trp Tyr Ile Tyr Glu Lys Gln  
95 100 105

Ala Leu Asp Asn Met Phe Ser Asn Lys Tyr Thr Trp Val Lys Tyr  
110 115 120

Asn Pro Leu Glu Ser Leu Ile Lys Asp Val Asp Trp Phe Leu Leu  
125 130 135

Gly Ser Pro Ile Glu Lys Leu Cys Lys His Ile Pro Leu Tyr Lys  
140 145 150

Gly Glu Val Val Glu Asn Thr His Asn Val Gly Ala Gly Gly Cys  
155 160 165

Ala Lys Ala Gly Leu Leu Gly Ile Leu Gly Ile Ser Ile Cys Ala  
170 175 180

Asp Ile His Val

<210> 222  
<211> 992  
<212> DNA  
<213> Homo sapiens

<400> 222  
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tgccagcagc ttctccaagg cacgggagga agaaattacc cctgtggtct 150  
ccattgcota caaagtcttg gaagttttcc ccaaaggccg ctgggtgctc 200  
ataacctgct gtgcacccca gccaccaccg cccatcacct attccctctg 250  
tggaaccaag aacatcaagg tggccaagaa ggtggtgaag acccagcagc 300  
cggcctcctt caacctcaac gtcacactca agtccagtcc agacctgctc 350  
acctacttct gccgggctgc ctccacctca ggtgcccattg tggacagtgc 400  
caggctacag atgcactggg agctgtggct caagccagtg tctgagctgc 450  
gggccaactt cactctgcag gacagagggg caggccccag ggtggagatg 500  
atctgccagg cgtcctcggg cagcccacct atcaccaaca gcctgatcgg 550  
gaaggatggg cagggtccacc tgcagcagag accatgccac aggcagcctg 600  
ccaacttctc cttctgccc agccagacat cggactgggt ctggtgccag 650  
gctgcaaaca acgccaatgt ccagcacagc gccctcacag tggtgccccc 700  
aggtggtgac cagaagatgg aggactggca gggccccctg gagagcccca 750  
tccttgccctt gccgctctac aggagcacc gccgtctgag tgaagaggag 800  
tttggggggt tcaggatagg gaatggggag gtcagaggac gcaaagcagc 850  
agccatgtag aatgaaccgt ccagagagcc aagcacggca gaggactgca 900

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[illegible]

<210> 224  
<211> 1297  
<212> DNA  
<213> Homo sapiens

<400> 224  
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ctctcttttgc tatgacatca ccgtcatccc taagttcaga cctggaccac 150  
gggtggtgtgc ggttcaaggc cagggtgatg aaaagacttt tcttcactat 200  
gactgtggca acaagacagt cacacctgtc agtcccctgg ggaagaaact 250  
aaatgtcaca acggcctgga aagcacagaa cccagtactg agagaggtgg 300  
tggacatact tacagagcaa ctgcgtgaca ttcagctgga gaattacaca 350  
cccaaggaac cctcaccct gcaggcaagg atgtcttgtg agcagaaagc 400  
tgaaggacac agcagtggat ctgggcagtt cagtttcgat gggcagatct 450  
tcctcctctt tgactcagag aagagaatgt ggacaacggt tcatcctgga 500  
gccagaaaga tgaaagaaaa gtgggagaat gacaagggtg tggccatgtc 550  
cttcattac ttctcaatgg gagactgtat aggatggctt gaggacttct 600  
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gagagtcctt tagagtgaac gggttaaagt gatacaaaa ggctcctgtg 800  
agcacggtct tgatcaaact cgcccttctg tctggccagc tgcccacgac 850  
ctacggtgta tgtccagtgg cctccagcag atcatgatga catcatggac 900  
ccaatagctc attcactgcc ttgattcctt ttgccaacaa ttttaccagc 950  
agttatacct aacatattat gcaattttct cttggtgcta cctgatggaa 1000  
ttcctgcact taaagttctg gctgactaaa caagatatat ctttttcttt 1050  
cttctctttt tgtttggaat atcaagtact tctttgaatg atgatctctt 1100  
tcttgcaaat gatattgtca gtaaaataat cacgttagac ttcagacctc 1150  
tggggattct ttccgtgtcc tgaaagagaa tttttaaatt atttaataag 1200  
aaaaaattta tattaatgat tgtttccttt agtaatttat tgttctgtac 1250  
tgatatttaa ataaagagtt ctatttccca aaaaaaaaaa aaaaaaa 1297

<210> 225  
<211> 246  
<212> PRT  
<213> Homo sapiens

<400> 225

Met Ala Ala Ala Ala Thr Lys Ile Leu Leu Cys Leu Pro Leu  
1 5 10 15  
Leu Leu Leu Leu Ser Gly Trp Ser Arg Ala Gly Arg Ala Asp Pro  
20 25 30  
His Ser Leu Cys Tyr Asp Ile Thr Val Ile Pro Lys Phe Arg Pro  
35 40 45  
Gly Pro Arg Trp Cys Ala Val Gln Gly Gln Val Asp Glu Lys Thr  
50 55 60  
Phe Leu His Tyr Asp Cys Gly Asn Lys Thr Val Thr Pro Val Ser  
65 70 75  
Pro Leu Gly Lys Lys Leu Asn Val Thr Thr Ala Trp Lys Ala Gln  
80 85 90  
Asn Pro Val Leu Arg Glu Val Val Asp Ile Leu Thr Glu Gln Leu  
95 100 105  
Arg Asp Ile Gln Leu Glu Asn Tyr Thr Pro Lys Glu Pro Leu Thr  
110 115 120  
Leu Gln Ala Arg Met Ser Cys Glu Gln Lys Ala Glu Gly His Ser  
125 130 135  
Ser Gly Ser Trp Gln Phe Ser Phe Asp Gly Gln Ile Phe Leu Leu  
140 145 150  
Phe Asp Ser Glu Lys Arg Met Trp Thr Thr Val His Pro Gly Ala  
155 160 165  
Arg Lys Met Lys Glu Lys Trp Glu Asn Asp Lys Val Val Ala Met  
170 175 180  
Ser Phe His Tyr Phe Ser Met Gly Asp Cys Ile Gly Trp Leu Glu  
185 190 195  
Asp Phe Leu Met Gly Met Asp Ser Thr Leu Glu Pro Ser Ala Gly  
200 205 210  
Ala Pro Leu Ala Met Ser Ser Gly Thr Thr Gln Leu Arg Ala Thr  
215 220 225  
Ala Thr Thr Leu Ile Leu Cys Cys Leu Leu Ile Ile Leu Pro Cys  
230 235 240  
Phe Ile Leu Pro Gly Ile  
245

<210> 226

<211> 735

<212> DNA

<213> Homo sapiens

<400> 226

gggaaagcca tttcgaaaac ccatctatac aaactatata ttttcatttc 50  
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caagttatat accgtggaat ggagttgatc ccaaccataa catcgtggag 150

gggttttaatt ttggtggtag ccctcaccca attctggtgt ggctttcttt 200  
 gcagaggatt ccaccttcaa aatcatgaac tctggctggt gatcaaaaga 250  
 gaatttggat tctactctaa aagtcaatat aggacttggc aaaagaagct 300  
 agcagaagac tcaacctggc ctcccataaa caggacagat tattcaggtg 350  
 atggcaaaaaa tggattctac atcaacggag gctatgaaag ccatgaacag 400  
 attccaaaaa gaaaactcaa attgggaggc caaccacag aacagcattt 450  
 ctgggccagg ctgtaatcag aattgtcgtc gtacatgctc aacagcattg 500  
 cttttttccc caaaattaac acattgtgga gaagtgatga tactctcccc 550  
 ttacctttcc tctctccatt caagcattca aagtatattt tcaatgaatt 600  
 aaaccttgca gcaagggacc ttagataggc ttattctgac tgtatgcttt 650  
 accaatgaga gaaaaaatg catttctgt atcatccttt tcaataaact 700  
 gtattcattt tgaaaaaaaa aaaaaaaaaa aaaaa 735

<210> 227  
 <211> 115  
 <212> PRT  
 <213> Homo sapiens

<400> 227  
 Met Glu Leu Ile Pro Thr Ile Thr Ser Trp Arg Val Leu Ile Leu  
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 Val Val Ala Leu Thr Gln Phe Trp Cys Gly Phe Leu Cys Arg Gly  
 20 25 30  
 Phe His Leu Gln Asn His Glu Leu Trp Leu Leu Ile Lys Arg Glu  
 35 40 45  
 Phe Gly Phe Tyr Ser Lys Ser Gln Tyr Arg Thr Trp Gln Lys Lys  
 50 55 60  
 Leu Ala Glu Asp Ser Thr Trp Pro Pro Ile Asn Arg Thr Asp Tyr  
 65 70 75  
 Ser Gly Asp Gly Lys Asn Gly Phe Tyr Ile Asn Gly Gly Tyr Glu  
 80 85 90  
 Ser His Glu Gln Ile Pro Lys Arg Lys Leu Lys Leu Gly Gly Gln  
 95 100 105  
 Pro Thr Glu Gln His Phe Trp Ala Arg Leu  
 110 115

<210> 228  
 <211> 2185  
 <212> DNA  
 <213> Homo sapiens

<400> 228  
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 cacaccatga agctcttgtg gcaggtaact gtgcaccacc acacctggaa 100

tgccatcctg ctcccgttcg tctacctcac ggcgcaagtg tggattctgt 150  
 gtgcagccat cgctgctgcc gcctcagccg ggccccagaa ctgccccctcc 200  
 gtttgctcgt gcagtaacca gttcagcaag gtggtgtgca cgcgcgcggg 250  
 cctctccgag gtcccgaggt gtattccctc gaacacccgg tacctcaacc 300  
 tcatggagaa caacatccag atgatccagg ccgacacctt ccgccacctc 350  
 caccacctgg aggtcctgca gttgggcagg aactccatcc ggcagattga 400  
 ggtggggggc ttcaacggcc tggccagcct caacaccctg gagctgttcg 450  
 acaactggct gacagtcata cctagcgggg cctttgaata cctgtccaag 500  
 ctgcgggagc tctggcttcg caacaacccc atcgaaagca tcccccttta 550  
 cgccttcaac cgggtgccct ccctcatgcg cctggacttg ggggagctca 600  
 agaagctgga gtatatctct gagggagctt ttgaggggct gttcaacctc 650  
 aagtatctga acttgggcat gtgcaacatt aaagacatgc ccaatctcac 700  
 cccccgttg gggctggagg agctggagat gtcagggaac cacttccctg 750  
 agatcagggc tggctccttc catggcctga gctccctcaa gaagctctgg 800  
 gtcatgaact cacaggtcag cctgattgag cggaatgctt ttgacgggct 850  
 ggoticaact gtggaactca acttggccca caataacctc tcttctttgc 900  
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 cacaacctt ggaactgtga ttgtgacatt ctgtggctag cctggtggct 1000  
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 coatgcacat gcgaggccgc tacctcgtgg aggtggacca ggcctccttc 1100  
 cagtgtcttg ccccttcat catggacgca cctcgagacc tcaacatttc 1150  
 tgagggctcg atggcagaac ttaagtgtcg gactccccct atgtcctccg 1200  
 tgaagtgggt gctgccaat gggacagtgc tcagccacgc ctcccgccac 1250  
 ccaaggatct ctgtcctcaa cgacggcacc ttgaactttt cccacgtgct 1300  
 gctttcagac actgggggtg acacatgcat ggtgaccaat gttgcaggca 1350  
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 tccaactaca gcttcttcac cacagtaaca gtggagacca cggagatctc 1450  
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 gttaccagcc ggcataatac acctctacca cgggtgtcat tcagactacc 1550  
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 cagcaacagc agctccgtcc ggtgtatcag gtgagggggc agtagtgctg 1850  
 cccacaatto atgaccatat taactacaac acctacaaac cagcacatgg 1900  
 ggcccactgg acagaaaaca gcctggggaa ctctctgcac cccacagtca 1950  
 ccactatctc tgaaccttat ataattcaga cccataccaa ggacaaggta 2000  
 caggaaactc aaatatgact cccctcccc aaaaaactta taaaatgcaa 2050  
 tagaatgcac acaaagacag caacttttgt acagagtggg gagagacttt 2100  
 ttcttgatata tgcttatata ttaagtctat gggctgggta aaaaaaacag 2150  
 attatattaa aatttaaaga caaaaagtca aaaca 2185

<210> 229  
 <211> 653  
 <212> PRT  
 <213> Homo sapiens

<400> 229  
 Met Lys Leu Leu Trp Gln Val Thr Val His His His Thr Trp Asn  
 1 5 10 15  
 Ala Ile Leu Leu Pro Phe Val Tyr Leu Thr Ala Gln Val Trp Ile  
 20 25 30  
 Leu Cys Ala Ala Ile Ala Ala Ala Ala Ser Ala Gly Pro Gln Asn  
 35 40 45  
 Cys Pro Ser Val Cys Ser Cys Ser Asn Gln Phe Ser Lys Val Val  
 50 55 60  
 Cys Thr Arg Arg Gly Leu Ser Glu Val Pro Gln Gly Ile Pro Ser  
 65 70 75  
 Asn Thr Arg Tyr Leu Asn Leu Met Glu Asn Asn Ile Gln Met Ile  
 80 85 90  
 Gln Ala Asp Thr Phe Arg His Leu His His Leu Glu Val Leu Gln  
 95 100 105  
 Leu Gly Arg Asn Ser Ile Arg Gln Ile Glu Val Gly Ala Phe Asn  
 110 115 120  
 Gly Leu Ala Ser Leu Asn Thr Leu Glu Leu Phe Asp Asn Trp Leu  
 125 130 135  
 Thr Val Ile Pro Ser Gly Ala Phe Glu Tyr Leu Ser Lys Leu Arg  
 140 145 150  
 Glu Leu Trp Leu Arg Asn Asn Pro Ile Glu Ser Ile Pro Ser Tyr  
 155 160 165  
 Ala Phe Asn Arg Val Pro Ser Leu Met Arg Leu Asp Leu Gly Glu  
 170 175 180  
 Leu Lys Lys Leu Glu Tyr Ile Ser Glu Gly Ala Phe Glu Gly Leu





500	505	510
Thr Thr Asp Lys Met Gln Thr Ser Leu	Asp Glu Val Met Lys Thr	
515	520	525
Thr Lys Ile Ile Ile Gly Cys Phe Val	Ala Val Thr Leu Leu Ala	
530	535	540
Ala Ala Met Leu Ile Val Phe Tyr Lys	Leu Arg Lys Arg His Gln	
545	550	555
Gln Arg Ser Thr Val Thr Ala Ala Arg	Thr Val Glu Ile Ile Gln	
560	565	570
Val Asp Glu Asp Ile Pro Ala Ala Thr	Ser Ala Ala Ala Thr Ala	
575	580	585
Ala Pro Ser Gly Val Ser Gly Glu Gly	Ala Val Val Leu Pro Thr	
590	595	600
Ile His Asp His Ile Asn Tyr Asn Thr	Tyr Lys Pro Ala His Gly	
605	610	615
Ala His Trp Thr Glu Asn Ser Leu Gly	Asn Ser Leu His Pro Thr	
620	625	630
Val Thr Thr Ile Ser Glu Pro Tyr Ile	Ile Gln Thr His Thr Lys	
635	640	645
Asp Lys Val Gln Glu Thr Gln Ile		
650		

<210> 230  
 <211> 2846  
 <212> DNA  
 <213> Homo sapiens

<400> 230  
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 tacacagtca ttaatgaagc ctgccctgga gcagagtgga atatcatgtg 150  
 tcgggagtgc tgtgaatatg atcagattga gtgcgtctgc cccggaaaga 200  
 gggaagtcgt gggttatacc atcccttgct gcaggaatga ggagaatgag 250  
 tgtgactcct gctgatcca ccaggttgt accatctttg aaaactgcaa 300  
 gagctgccga aatggctcat ggggggttac cttggatgac ttctatgtga 350  
 aggggttcta ctgtgcagag tgccgagcag gctggtacgg aggagactgc 400  
 atgcgatgtg gccaggttct gcgagcccca aagggtcaga ttttgttgga 450  
 aagctatccc ctaaagtctc actgtgaatg gaccattcat gctaaacctg 500  
 ggtttgcac ccaactaaga tttgtcatgt tgagtctgga gtttgactac 550  
 atgtgccagt atgactatgt tgaggttcgt gatggagaca accgcgatgg 600  
 ccagatcatc aagcgtgtct gtggcaacga gcggccagct cctatccaga 650

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tgaagcagtg tgggcctgaa gtgtgatttg gcctgtgaac ttggctgtgc 2300  
cagggcttct gacttcaggg acaaaactca gtgaaggggtg agtagacctc 2350  
cattgctggg aggctgatgc cgcgtccact actaggacag ccaattggaa 2400  
gatgccaggg cttgcaagaa gtaagtttct tcaaagaaga ccatatacaa 2450  
aacctctcca ctccactgac ctgggtgtct tccccaactt tcagttatac 2500  
gaatgccatc agcttgacca gggaagatct gggcttcattg agggcccttt 2550  
tgaggctctc aagttctaga gagctgcctg tgggacagcc cagggcagca 2600  
gagctgggat gtggtgcatg cctttgtgta catggccaca gtacagtctg 2650  
gtccttttcc ttcccatct cttgtacaca ttttaataaa ataagggttg 2700  
gcttctgaac tacaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2750  
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<210> 231  
<211> 720  
<212> PRT  
<213> Homo sapiens

<400> 231  
Met Glu Leu Gly Cys Trp Thr Gln Leu Gly Leu Thr Phe Leu Gln  
1 5 10 15  
Leu Leu Leu Ile Ser Ser Leu Pro Arg Glu Tyr Thr Val Ile Asn  
20 25 30  
Glu Ala Cys Pro Gly Ala Glu Trp Asn Ile Met Cys Arg Glu Cys  
35 40 45  
Cys Glu Tyr Asp Gln Ile Glu Cys Val Cys Pro Gly Lys Arg Glu  
50 55 60  
Val Val Gly Tyr Thr Ile Pro Cys Cys Arg Asn Glu Glu Asn Glu  
65 70 75  
Cys Asp Ser Cys Leu Ile His Pro Gly Cys Thr Ile Phe Glu Asn  
80 85 90  
Cys Lys Ser Cys Arg Asn Gly Ser Trp Gly Gly Thr Leu Asp Asp  
95 100 105  
Phe Tyr Val Lys Gly Phe Tyr Cys Ala Glu Cys Arg Ala Gly Trp  
110 115 120  
Tyr Gly Gly Asp Cys Met Arg Cys Gly Gln Val Leu Arg Ala Pro  
125 130 135  
Lys Gly Gln Ile Leu Leu Glu Ser Tyr Pro Leu Asn Ala His Cys  
140 145 150  
Glu Trp Thr Ile His Ala Lys Pro Gly Phe Val Ile Gln Leu Arg  
155 160 165

Phe	Val	Met	Leu	Ser	Leu	Glu	Phe	Asp	Tyr	Met	Cys	Gln	Tyr	Asp	
				170					175					180	
Tyr	Val	Glu	Val	Arg	Asp	Gly	Asp	Asn	Arg	Asp	Gly	Gln	Ile	Ile	
				185					190					195	
Lys	Arg	Val	Cys	Gly	Asn	Glu	Arg	Pro	Ala	Pro	Ile	Gln	Ser	Ile	
				200					205					210	
Gly	Ser	Ser	Leu	His	Val	Leu	Phe	His	Ser	Asp	Gly	Ser	Lys	Asn	
				215					220					225	
Phe	Asp	Gly	Phe	His	Ala	Ile	Tyr	Glu	Glu	Ile	Thr	Ala	Cys	Ser	
				230					235					240	
Ser	Ser	Pro	Cys	Phe	His	Asp	Gly	Thr	Cys	Val	Leu	Asp	Lys	Ala	
				245					250					255	
Gly	Ser	Tyr	Lys	Cys	Ala	Cys	Leu	Ala	Gly	Tyr	Thr	Gly	Gln	Arg	
				260					265					270	
Cys	Glu	Asn	Leu	Leu	Glu	Glu	Arg	Asn	Cys	Ser	Asp	Pro	Gly	Gly	
				275					280					285	
Pro	Val	Asn	Gly	Tyr	Gln	Lys	Ile	Thr	Gly	Gly	Pro	Gly	Leu	Ile	
				290					295					300	
Asn	Gly	Arg	His	Ala	Lys	Ile	Gly	Thr	Val	Val	Ser	Phe	Phe	Cys	
				305					310					315	
Asn	Asn	Ser	Tyr	Val	Leu	Ser	Gly	Asn	Glu	Lys	Arg	Thr	Cys	Gln	
				320					325					330	
Gln	Asn	Gly	Glu	Trp	Ser	Gly	Lys	Gln	Pro	Ile	Cys	Ile	Lys	Ala	
				335					340					345	
Cys	Arg	Glu	Pro	Lys	Ile	Ser	Asp	Leu	Val	Arg	Arg	Arg	Val	Leu	
				350					355					360	
Pro	Met	Gln	Val	Gln	Ser	Arg	Glu	Thr	Pro	Leu	His	Gln	Leu	Tyr	
				365					370					375	
Ser	Ala	Ala	Phe	Ser	Lys	Gln	Lys	Leu	Gln	Ser	Ala	Pro	Thr	Lys	
				380					385					390	
Lys	Pro	Ala	Leu	Pro	Phe	Gly	Asp	Leu	Pro	Met	Gly	Tyr	Gln	His	
				395					400					405	
Leu	His	Thr	Gln	Leu	Gln	Tyr	Glu	Cys	Ile	Ser	Pro	Phe	Tyr	Arg	
				410					415					420	
Arg	Leu	Gly	Ser	Ser	Arg	Arg	Thr	Cys	Leu	Arg	Thr	Gly	Lys	Trp	
				425					430					435	
Ser	Gly	Arg	Ala	Pro	Ser	Cys	Ile	Pro	Ile	Cys	Gly	Lys	Ile	Glu	
				440					445					450	
Asn	Ile	Thr	Ala	Pro	Lys	Thr	Gln	Gly	Leu	Arg	Trp	Pro	Trp	Gln	
				455					460					465	
Ala	Ala	Ile	Tyr	Arg	Arg	Thr	Ser	Gly	Val	His	Asp	Gly	Ser	Leu	
				470					475					480	

His	Lys	Gly	Ala	Trp	Phe	Leu	Val	Cys	Ser	Gly	Ala	Leu	Val	Asn	485	490	495
Glu	Arg	Thr	Val	Val	Val	Ala	Ala	His	Cys	Val	Thr	Asp	Leu	Gly	500	505	510
Lys	Val	Thr	Met	Ile	Lys	Thr	Ala	Asp	Leu	Lys	Val	Val	Leu	Gly	515	520	525
Lys	Phe	Tyr	Arg	Asp	Asp	Asp	Arg	Asp	Glu	Lys	Thr	Ile	Gln	Ser	530	535	540
Leu	Gln	Ile	Ser	Ala	Ile	Ile	Leu	His	Pro	Asn	Tyr	Asp	Pro	Ile	545	550	555
Leu	Leu	Asp	Ala	Asp	Ile	Ala	Ile	Leu	Lys	Leu	Leu	Asp	Lys	Ala	560	565	570
Arg	Ile	Ser	Thr	Arg	Val	Gln	Pro	Ile	Cys	Leu	Ala	Ala	Ser	Arg	575	580	585
Asp	Leu	Ser	Thr	Ser	Phe	Gln	Glu	Ser	His	Ile	Thr	Val	Ala	Gly	590	595	600
Trp	Asn	Val	Leu	Ala	Asp	Val	Arg	Ser	Pro	Gly	Phe	Lys	Asn	Asp	605	610	615
Thr	Leu	Arg	Ser	Gly	Val	Val	Ser	Val	Val	Asp	Ser	Leu	Leu	Cys	620	625	630
Glu	Glu	Gln	His	Glu	Asp	His	Gly	Ile	Pro	Val	Ser	Val	Thr	Asp	635	640	645
Asn	Met	Phe	Cys	Ala	Ser	Trp	Glu	Pro	Thr	Ala	Pro	Ser	Asp	Ile	650	655	660
Cys	Thr	Ala	Glu	Thr	Gly	Gly	Ile	Ala	Ala	Val	Ser	Phe	Pro	Gly	665	670	675
Arg	Ala	Ser	Pro	Glu	Pro	Arg	Trp	His	Leu	Met	Gly	Leu	Val	Ser	680	685	690
Trp	Ser	Tyr	Asp	Lys	Thr	Cys	Ser	His	Arg	Leu	Ser	Thr	Ala	Phe	695	700	705
Thr	Lys	Val	Leu	Pro	Phe	Lys	Asp	Trp	Ile	Glu	Arg	Asn	Met	Lys	710	715	720

<210> 232

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 232

agggttcgtga tggagacaac cgcg 24

<210> 233

<211> 24

<212> DNA

<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 233  
tgtcaaggac gcactgccgt catg 24

<210> 234  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 234  
tggccagatc atcaagcgtg tctgtggcaa cgagcggcca gtcctatcc 50

<210> 235  
<211> 1964  
<212> DNA  
<213> Homo sapiens

<400> 235  
accaggcatt gtatcttcag ttgtcatcaa gttcgcaatc agattggaaa 50  
agctcaactt gaagctttct tgcctgcagt gaagcagaga gatagatatt 100  
attcacgtaa taaaaaacat gggcttcaac ctgactttcc acctttccta 150  
caaattccga ttactgttgc tgttgacttt gtgcctgaca gtggttgggt 200  
gggccaccag taactacttc gtgggtgccca ttcaagagat tcctaaagca 250  
aaggagttca tggctaattt ccataagacc ctcatttttg ggaagggaaa 300  
aactctgact aatgaagcat ccacgaagaa ggtagaactt gacaactgtc 350  
cttctgtgtc tccttacctc agaggccaga gcaagctcat tttcaaacca 400  
gatctcactt tggaagaggt acaggcagaa aatcccaaag tgtccagagg 450  
ccggtatcgc cctcaggaat gtaaagcttt acagagggtc gccatcctcg 500  
ttccccaccg gaacagagag aaacacctga tgtacctgct ggaacatctg 550  
catcccttcc tgcagaggca gcagctggat tatggcatct acgtcatcca 600  
ccaggctgaa ggtaaaaagt ttaatcgagc caaactcttg aatgtgggct 650  
atctagaagc cctcaaggaa gaaaattggg actgctttat attccacgat 700  
gtggacctgg tacccgagaa tgactttaac ctttacaagt gtgaggagca 750  
tccaagcat ctggtgggtg gcaggaacag cactgggtac aggttacgtt 800  
acagtggata ttttgggggt gttactgccc taagcagaga gcagtttttc 850  
aagggtgaatg gattctctaa caactactgg ggatggggag gcgaagacga 900  
tgacctcaga ctcagggttg agctccaaag aatgaaaatt tcccggcccc 950  
tgcctgaagt gggtaaatat acaatggtct tccacactag agacaaaggc 1000

aatgaggtga acgcagaacg gatgaagctc ttacaccaag tgtcacgagt 1050  
ctggagaaca gatgggttga gtagttgttc ttataaatta gtatctgttg 1100  
aacacaatcc tttatatatc aacatcacag tggatttctg gtttggtgca 1150  
tgaccctgga tcttttgggtg atgtttggaa gaactgattc tttgtttgca 1200  
ataatttttg cctagagact tcaaatagta gcacacatta agaacctgtt 1250  
acagctcatt gttgagctga atttttcctt tttgtatttt cttagcagag 1300  
ctcctggtga tgtagagtat aaaacagttg taacaagaca gctttcttag 1350  
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ttatataaaa ggatgactca aaggataaaa tgaacgctat ttgaggactc 1450  
tggttgaagg agatttattt aaatttgaag taatatatta tgggataaaa 1500  
ggccacagga aataagactg ctgaatgtct gagagaacca gagttgttct 1550  
cgtccaaggt agaaaggtag gaagatacaa tactgttatt catttatcct 1600  
gtacaatcat ctgtgaagtg gtggtgtcag gtgagaaggc gtccacaaaa 1650  
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cagtgatgcc caccagagaa tacattctct attagttttt aaagagtttt 1850  
tgtaaaatga ttttgtacaa gtaggatatg aattagcagt ttacaagttt 1900  
acatattaac taataataaa tatgtctatc aaatacctct gtagtaaaat 1950  
gtgaaaaagc aaaa 1964

<210> 236

<211> 344

<212> PRT

<213> Homo sapiens

<220>

<221> Signal peptide

<222> 1-27

<223> Signal peptide

<220>

<221> N-glycosylation sites

<222> 4-7, 220-223, 335-338

<223> N-glycosylation sites

<220>

<221> Xylose isomerase proteins

<222> 191-201

<223> Xylose isomerase proteins

<400> 236

Met	Gly	Phe	Asn	Leu	Thr	Phe	His	Leu	Ser	Tyr	Lys	Phe	Arg	Leu
1					5					10				15



Leu	Leu	Leu	Leu	Thr	Leu	Cys	Leu	Thr	Val	Val	Gly	Trp	Ala	Thr		20	25	30
Ser	Asn	Tyr	Phe	Val	Gly	Ala	Ile	Gln	Glu	Ile	Pro	Lys	Ala	Lys		35	40	45
Glu	Phe	Met	Ala	Asn	Phe	His	Lys	Thr	Leu	Ile	Leu	Gly	Lys	Gly		50	55	60
Lys	Thr	Leu	Thr	Asn	Glu	Ala	Ser	Thr	Lys	Lys	Val	Glu	Leu	Asp		65	70	75
Asn	Cys	Pro	Ser	Val	Ser	Pro	Tyr	Leu	Arg	Gly	Gln	Ser	Lys	Leu		80	85	90
Ile	Phe	Lys	Pro	Asp	Leu	Thr	Leu	Glu	Glu	Val	Gln	Ala	Glu	Asn		95	100	105
Pro	Lys	Val	Ser	Arg	Gly	Arg	Tyr	Arg	Pro	Gln	Glu	Cys	Lys	Ala		110	115	120
Leu	Gln	Arg	Val	Ala	Ile	Leu	Val	Pro	His	Arg	Asn	Arg	Glu	Lys		125	130	135
His	Leu	Met	Tyr	Leu	Leu	Glu	His	Leu	His	Pro	Phe	Leu	Gln	Arg		140	145	150
Gln	Gln	Leu	Asp	Tyr	Gly	Ile	Tyr	Val	Ile	His	Gln	Ala	Glu	Gly		155	160	165
Lys	Ly's	Phe	Asn	Arg	Ala	Lys	Leu	Leu	Asn	Val	Gly	Tyr	Leu	Glu		170	175	180
Ala	Leu	Lys	Glu	Glu	Asn	Trp	Asp	Cys	Phe	Ile	Phe	His	Asp	Val		185	190	195
Asp	Leu	Val	Pro	Glu	Asn	Asp	Phe	Asn	Leu	Tyr	Lys	Cys	Glu	Glu		200	205	210
His	Pro	Lys	His	Leu	Val	Val	Gly	Arg	Asn	Ser	Thr	Gly	Tyr	Arg		215	220	225
Leu	Arg	Tyr	Ser	Gly	Tyr	Phe	Gly	Gly	Val	Thr	Ala	Leu	Ser	Arg		230	235	240
Glu	Gln	Phe	Phe	Lys	Val	Asn	Gly	Phe	Ser	Asn	Asn	Tyr	Trp	Gly		245	250	255
Trp	Gly	Gly	Glu	Asp	Asp	Asp	Leu	Arg	Leu	Arg	Val	Glu	Leu	Gln		260	265	270
Arg	Met	Lys	Ile	Ser	Arg	Pro	Leu	Pro	Glu	Val	Gly	Lys	Tyr	Thr		275	280	285
Met	Val	Phe	His	Thr	Arg	Asp	Lys	Gly	Asn	Glu	Val	Asn	Ala	Glu		290	295	300
Arg	Met	Lys	Leu	Leu	His	Gln	Val	Ser	Arg	Val	Trp	Arg	Thr	Asp		305	310	315
Gly	Leu	Ser	Ser	Cys	Ser	Tyr	Lys	Leu	Val	Ser	Val	Glu	His	Asn		320	325	330

Pro Leu Tyr Ile Asn Ile Thr Val Asp Phe Trp Phe Gly Ala  
 335 340

<210> 237  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 237  
 ccttacctca gaggccagag caagc 25

<210> 238  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 238  
 gagcttcacgc cgttctgcgt tcacc 25

<210> 239  
 <211> 46  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 239  
 caggaatgta aagctttaca gagggtcgcc atcctcgttc cccacc 46

<210> 240  
 <211> 2567  
 <212> DNA  
 <213> Homo sapiens

<400> 240  
 cgtggggccgg ggtcgcgcag cgggctgtgg gcgcgcccgg aggagcgacc 50  
 gccgcagttc tcgagctcca gctgcattcc ctccgcgtcc gccccacgct 100  
 tctcccgtc cgggccccgc aatggcccag gcagtgtggt cgcgcctcgg 150  
 ccgcacctc tggcttgctt gctcctgcc ctgggccccg gcaggggtgg 200  
 ccgcaggcct gtatgaactc aatctcacca ccgatagccc tgccaccacg 250  
 ggagcgggtg tgaccatctc ggccagcctg gtggccaagg acaacggcag 300  
 cctggccctg cccgctgacg cccacctcta ccgcttcac tgcatccaca 350  
 ccccgtggt gcttactggc aagatggaga agggctcag ctccaccatc 400  
 cgtgtggtcg gccacgtgcc cggggaattc ccggtctctg tctgggtcac 450  
 tgccgctgac tgctggatgt gccagcctgt ggccaggggc tttgtggtcc 500  
 tccccatcac agagttcctc gtgggggacc ttgttgtcac ccagaacact 550

tccctaccct ggcccagctc ctatctcact aagaccgtcc tgaaagtctc 600  
 cttcctcctc cagcaccga gcaacttcct caagaccgcc ttgtttctct 650  
 acagctggga cttcggggac gggaccaga tggtgactga agactccgtg 700  
 gtctattata actattccat catcgggacc ttcaccgtga agctcaaagt 750  
 ggtggcggag tgggaagagg tggagccgga tgccacgagg gctgtgaagc 800  
 agaagaccgg ggactttctc gcctcgtga agctgcagga aacccttoga 850  
 ggcacccaag tgttggggcc caccctaatt cagaccttcc aaaagatgac 900  
 cgtgaccttg aacttcctgg ggagccctcc tctgactgtg tgctggcgtc 950  
 tcaagcctga gtgcctccc ctggaggaag gggagtcca ccctgtgtcc 1000  
 gtggccagca cagcgtacaa cctgaccac accttcaggg accctgggga 1050  
 ctactgcttc agcatccggg ccgagaatat catcagcaag acacatcagt 1100  
 accacaagat ccaggtgtgg ccctccagaa tccagccggc tgtctttgct 1150  
 ttccatgtg ctacacttat cactgtgatg ttggccttca tcatgtacat 1200  
 gaccctgogg aatgccactc agcaaaagga catggtggag aaccgggagc 1250  
 caccctctgg ggtcaggtgc tgctgccaga tgtgctgtgg gcctttcttg 1300  
 ctggagactc catctgagta cctggaaatt gttcgtgaga accacgggct 1350  
 gctcccgccc ctctataagt ctgtcaaac ttacaccgtg tgagcactcc 1400  
 ccctccccac cccatctcag tgttaactga ctgctgactt ggagtttcca 1450  
 gcagggtggt gtgcaccact gaccaggagg ggttcatttg cgtggggctg 1500  
 ttggcctgga tcatccatcc atctgtacag ttcagccact gccacaagcc 1550  
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 cagccactga cataagcccc actcggttac cacccttg acccctacc 1650  
 tttgaagagg cttcgtgcag gactttgatg cttgggggtg tccgtgttga 1700  
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 gtgccagaga gctagaaaga aggtcataaa ggggttaaaaa tccataacta 1850  
 aaggtgttac acatagatgg gcacactcac agagagaagt gtgcatgtac 1900  
 acacaccaca cacacacaca cacacacaca cacagaaata taaacacatg 1950  
 cgtcacatgg gcatttcaga tgatcagctc tgtatctggt taagtcgggt 2000  
 gctgggatgc accctgcact agagctgaaa ggaaatttga cctccaagca 2050  
 gccctgacag gttctgggcc cgggccctcc ctttgtgctt tgtctctgca 2100  
 gttcttgccg cctttataag gccatcctag tccctgctgg ctggcagggg 2150

cctggatggg gggcaggact aatactgagt gattgcagag tgctttataa 2200  
 atatcacctt attttatcga aacccatctg tgaaaactttc actgaggaaa 2250  
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 aogcctgtaa tcccagcact ttgggaggcc gaggcgggtg gatcacgaga 2350  
 tcaggagatc gagaccaccc tggctaacac ggtgaaaccc cgtctctact 2400  
 aaaaaaatac aaaaagttag ccgggcgtgg tgggtgggtgc ctgtagtccc 2450  
 agctactcgg gaggctgagg caggagaatg gtgcgaaccc gggaggcgga 2500  
 gcttgcagtg agcccagatg gcgccactgc actccagcct gagtgcacaga 2550  
 gcgagactct gtctcca 2567

<210> 241

<211> 423

<212> PRT

<213> Homo sapiens

<400> 241

Met	Ala	Gln	Ala	Val	Trp	Ser	Arg	Leu	Gly	Arg	Ile	Leu	Trp	Leu	1	5	10	15
Ala	Cys	Leu	Leu	Pro	Trp	Ala	Pro	Ala	Gly	Val	Ala	Ala	Gly	Leu	20	25	30	
Tyr	Glu	Leu	Asn	Leu	Thr	Thr	Asp	Ser	Pro	Ala	Thr	Thr	Gly	Ala	35	40	45	
Val	Val	Thr	Ile	Ser	Ala	Ser	Leu	Val	Ala	Lys	Asp	Asn	Gly	Ser	50	55	60	
Leu	Ala	Leu	Pro	Ala	Asp	Ala	His	Leu	Tyr	Arg	Phe	His	Trp	Ile	65	70	75	
His	Thr	Pro	Leu	Val	Leu	Thr	Gly	Lys	Met	Glu	Lys	Gly	Leu	Ser	80	85	90	
Ser	Thr	Ile	Arg	Val	Val	Gly	His	Val	Pro	Gly	Glu	Phe	Pro	Val	95	100	105	
Ser	Val	Trp	Val	Thr	Ala	Ala	Asp	Cys	Trp	Met	Cys	Gln	Pro	Val	110	115	120	
Ala	Arg	Gly	Phe	Val	Val	Leu	Pro	Ile	Thr	Glu	Phe	Leu	Val	Gly	125	130	135	
Asp	Leu	Val	Val	Thr	Gln	Asn	Thr	Ser	Leu	Pro	Trp	Pro	Ser	Ser	140	145	150	
Tyr	Leu	Thr	Lys	Thr	Val	Leu	Lys	Val	Ser	Phe	Leu	Leu	His	Asp	155	160	165	
Pro	Ser	Asn	Phe	Leu	Lys	Thr	Ala	Leu	Phe	Leu	Tyr	Ser	Trp	Asp	170	175	180	
Phe	Gly	Asp	Gly	Thr	Gln	Met	Val	Thr	Glu	Asp	Ser	Val	Val	Tyr	185	190	195	

Tyr	Asn	Tyr	Ser	Ile	Ile	Gly	Thr	Phe	Thr	Val	Lys	Leu	Lys	Val
				200					205					210
Val	Ala	Glu	Trp	Glu	Glu	Val	Glu	Pro	Asp	Ala	Thr	Arg	Ala	Val
				215					220					225
Lys	Gln	Lys	Thr	Gly	Asp	Phe	Ser	Ala	Ser	Leu	Lys	Leu	Gln	Glu
				230					235					240
Thr	Leu	Arg	Gly	Ile	Gln	Val	Leu	Gly	Pro	Thr	Leu	Ile	Gln	Thr
				245					250					255
Phe	Gln	Lys	Met	Thr	Val	Thr	Leu	Asn	Phe	Leu	Gly	Ser	Pro	Pro
				260					265					270
Leu	Thr	Val	Cys	Trp	Arg	Leu	Lys	Pro	Glu	Cys	Leu	Pro	Leu	Glu
				275					280					285
Glu	Gly	Glu	Cys	His	Pro	Val	Ser	Val	Ala	Ser	Thr	Ala	Tyr	Asn
				290					295					300
Leu	Thr	His	Thr	Phe	Arg	Asp	Pro	Gly	Asp	Tyr	Cys	Phe	Ser	Ile
				305					310					315
Arg	Ala	Glu	Asn	Ile	Ile	Ser	Lys	Thr	His	Gln	Tyr	His	Lys	Ile
				320					325					330
Gln	Val	Trp	Pro	Ser	Arg	Ile	Gln	Pro	Ala	Val	Phe	Ala	Phe	Pro
				335					340					345
Cys	Ala	Thr	Leu	Ile	Thr	Val	Met	Leu	Ala	Phe	Ile	Met	Tyr	Met
				350					355					360
Thr	Leu	Arg	Asn	Ala	Thr	Gln	Gln	Lys	Asp	Met	Val	Glu	Asn	Pro
				365					370					375
Glu	Pro	Pro	Ser	Gly	Val	Arg	Cys	Cys	Cys	Gln	Met	Cys	Cys	Gly
				380					385					390
Pro	Phe	Leu	Leu	Glu	Thr	Pro	Ser	Glu	Tyr	Leu	Glu	Ile	Val	Arg
				395					400					405
Glu	Asn	His	Gly	Leu	Leu	Pro	Pro	Leu	Tyr	Lys	Ser	Val	Lys	Thr
				410					415					420

Thr Thr Val

<210> 242  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 242  
 catttcctta ccctggaccc agctcc 26  
  
 <210> 243  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 243  
gaaaggccca cagcacatct ggcag 25

<210> 244  
<211> 46  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 244  
ccacgacccg agcaacttcc tcaagaccga cttgtttctc tacagc 46

<210> 245  
<211> 485  
<212> DNA  
<213> Homo sapiens

<400> 245  
gctcaagacc cagcagtggg acagccagac agacggcacg atggcactga 50  
gctccagat ctgggcoctg tgcctcctgc tcctcctcct cctcgccagc 100  
ctgaccagtg gctctgtttt ccacaaacag acgggacaac ttgcagagct 150  
gcaaccccag gacagagctg gagccagggc cagctggatg cccatgttcc 200  
agaggcgaag gaggcgagac acccacttcc ccactctgcat tttctgctgc 250  
ggctgctgtc atcgatcaaa gtgtgggatg tgctgcaaga cgtagaacct 300  
acctgccctg ccccgctccc ctcccttctt tatttattcc tgctgcccc 350  
gaacataggt cttggaataa aatggctggg tcttttgttt tccccaaaaa 400  
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 450  
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 485

<210> 246  
<211> 84  
<212> PRT  
<213> Homo sapiens

<400> 246  
Met Ala Leu Ser Ser Gln Ile Trp Ala Ala Cys Leu Leu Leu Leu  
1 5 10 15  
Leu Leu Leu Ala Ser Leu Thr Ser Gly Ser Val Phe Pro Gln Gln  
20 25 30  
Thr Gly Gln Leu Ala Glu Leu Gln Pro Gln Asp Arg Ala Gly Ala  
35 40 45  
Arg Ala Ser Trp Met Pro Met Phe Gln Arg Arg Arg Arg Arg Asp  
50 55 60  
Thr His Phe Pro Ile Cys Ile Phe Cys Cys Gly Cys Cys His Arg  
65 70 75

Ser Lys Cys Gly Met Cys Cys Lys Thr  
80

<210> 247  
<211> 2359  
<212> DNA  
<213> Homo sapiens

<400> 247  
ctgtcaggaa ggaccatctg aaggctgcaa tttgttctta gggaggcagg 50  
tgctggcctg gcctggatct tccaccatgt tcctgttgct gccttttgat 100  
agcctgattg tcaaccttct gggcatctcc ctgactgtcc tcttcaccct 150  
ccttctcggtt ttcatcatag tgccagccat ttttgagatc tcctttggta 200  
tccgcaaact ctacatgaaa agtctgttaa aaatctttgc gtgggctacc 250  
ttgagaatgg agcgaggagc caaggagaag aaccaccagc tttacaagcc 300  
ctacaccaac ggaatcattg caaaggatcc cacttcacta gaagaagaga 350  
tcaaagagat tcgtcgaagt ggtagtagta aggctctgga caacactcca 400  
gagttcgagc tctctgacat tttctacttt tgccggaaag gaatggagac 450  
cattatggat gatgaggtga caaagagatt ctcagcagaa gaactggagt 500  
cctggaacct gctgagcaga accaattata acttcagta catcagcctt 550  
cggctcacgg tcctgtgggg gttaggagtg ctgattcggg actgctttct 600  
gctgccgctc aggatagcac tggttttcac agggattagc cttctggtgg 650  
tgggcacaac tgtggtggga tacttgocaa atgggaggtt taaggaattc 700  
atgagtaaac atgttcactt aatgtgttac cggatctgcg tgcgagcgct 750  
gacagccatc atcacctacc atgacaggga aaacagacca agaaatggtg 800  
gcatctgtgt ggccaatcat acctcacoga tcgatgtgat catcttggcc 850  
agcgatggct attatgccat ggtgggtcaa gtgcacgggg gactcatggg 900  
tgtgattcag agagccatgg tgaaggcctg cccacacgtc tggtttgagc 950  
gctcggaagt gaaggatcgc cacctggtgg ctaagagact gactgaacat 1000  
gtgcaagata aaagcaagct gcctatcctc atcttcccag aaggaaacctg 1050  
catcaataat acatcggtga tgatgttcaa aaagggaagt tttgaaattg 1100  
gagccacagt ttacctgtt gctatcaagt atgacctca atttggcgat 1150  
gccttctgga acagcagcaa atacgggatg gtgacgtacc tgctgcgaat 1200  
gatgaccagc tgggccattg tctgcagcgt gtggtacctg cctcccatga 1250  
ctagagaggc agatgaagat gctgtccagt ttgcgaatag ggtgaaatct 1300  
gccattgcca ggcaggagg acttgtggac ctgctgtggg atgggggcct 1350





Tyr	Thr	Asn	Gly	Ile 80	Ile	Ala	Lys	Asp	Pro 85	Thr	Ser	Leu	Glu	Glu 90
Glu	Ile	Lys	Glu	Ile 95	Arg	Arg	Ser	Gly	Ser 100	Ser	Lys	Ala	Leu	Asp 105
Asn	Thr	Pro	Glu	Phe 110	Glu	Leu	Ser	Asp	Ile 115	Phe	Tyr	Phe	Cys	Arg 120
Lys	Gly	Met	Glu	Thr 125	Ile	Met	Asp	Asp	Glu 130	Val	Thr	Lys	Arg	Phe 135
Ser	Ala	Glu	Glu	Leu 140	Glu	Ser	Trp	Asn	Leu 145	Leu	Ser	Arg	Thr	Asn 150
Tyr	Asn	Phe	Gln	Tyr 155	Ile	Ser	Leu	Arg	Leu 160	Thr	Val	Leu	Trp	Gly 165
Leu	Gly	Val	Leu	Ile 170	Arg	Tyr	Cys	Phe	Leu 175	Leu	Pro	Leu	Arg	Ile 180
Ala	Leu	Ala	Phe	Thr 185	Gly	Ile	Ser	Leu	Leu 190	Val	Val	Gly	Thr	Thr 195
Val	Val	Gly	Tyr	Leu 200	Pro	Asn	Gly	Arg	Phe 205	Lys	Glu	Phe	Met	Ser 210
Lys	His	Val	His	Leu 215	Met	Cys	Tyr	Arg	Ile 220	Cys	Val	Arg	Ala	Leu 225
Thr	Ala	Ile	Ile	Thr 230	Tyr	His	Asp	Arg	Glu 235	Asn	Arg	Pro	Arg	Asn 240
Gly	Gly	Ile	Cys	Val 245	Ala	Asn	His	Thr	Ser 250	Pro	Ile	Asp	Val	Ile 255
Ile	Leu	Ala	Ser	Asp 260	Gly	Tyr	Tyr	Ala	Met 265	Val	Gly	Gln	Val	His 270
Gly	Gly	Leu	Met	Gly 275	Val	Ile	Gln	Arg	Ala 280	Met	Val	Lys	Ala	Cys 285
Pro	His	Val	Trp	Phe 290	Glu	Arg	Ser	Glu	Val 295	Lys	Asp	Arg	His	Leu 300
Val	Ala	Lys	Arg	Leu 305	Thr	Glu	His	Val	Gln 310	Asp	Lys	Ser	Lys	Leu 315
Pro	Ile	Leu	Ile	Phe 320	Pro	Glu	Gly	Thr	Cys 325	Ile	Asn	Asn	Thr	Ser 330
Val	Met	Met	Phe	Lys 335	Lys	Gly	Ser	Phe	Glu 340	Ile	Gly	Ala	Thr	Val 345
Tyr	Pro	Val	Ala	Ile 350	Lys	Tyr	Asp	Pro	Gln 355	Phe	Gly	Asp	Ala	Phe 360
Trp	Asn	Ser	Ser	Lys 365	Tyr	Gly	Met	Val	Thr 370	Tyr	Leu	Leu	Arg	Met 375
Met	Thr	Ser	Trp	Ala 380	Ile	Val	Cys	Ser	Val 385	Trp	Tyr	Leu	Pro	Pro 390

Met	Thr	Arg	Glu	Ala	Asp	Glu	Asp	Ala	Val	Gln	Phe	Ala	Asn	Arg
				395					400					405
Val	Lys	Ser	Ala	Ile	Ala	Arg	Gln	Gly	Gly	Leu	Val	Asp	Leu	Leu
				410					415					420
Trp	Asp	Gly	Gly	Leu	Lys	Arg	Glu	Lys	Val	Lys	Asp	Thr	Phe	Lys
				425					430					435
Glu	Glu	Gln	Gln	Lys	Leu	Tyr	Ser	Lys	Met	Ile	Val	Gly	Asn	His
				440					445					450
Lys	Asp	Arg	Ser	Arg	Ser									
				455										

<210> 249  
 <211> 1103  
 <212> DNA  
 <213> Homo sapiens

<400> 249  
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 gccctcggca gcctcggcct ccacacctgg caggcccagg ctgttccac 150  
 catcctgccc ctgggcctgg ctccagacac ctttgacgat acctatgtgg 200  
 gttgtgcaga ggagatggag gagaaggcag cccccctgct aaaggaggaa 250  
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 ctgggaggac aagcgtcgag ggcttacctt gccccctggc ttcaaagccc 350  
 agaatggaat agccattatg gtctacacca actcatcgaa caccttgtac 400  
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 catgaggcac tttcccttca aggccctgca tttctacctg atccgggccc 500  
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 acgaagaggc acctccagca gccttgagaa gcaagaacat ggttccggac 900  
 ccagccctag cagccttctc cccaaccagg atgttggcct ggggaggcca 950  
 cagcagggtg gagggaaact tgctatgtga tggggacttc ctgggacaag 1000  
 caaggaaagt actgaggcag ccacttgatt gaacggtgtt gcaatgtgga 1050

gacatggagt tttattgagg tagctacgtg attaaatggt attgcagtgt 1100

gga 1103

<210> 250

<211> 240

<212> PRT

<213> Homo sapiens

<400> 250

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His	Thr	Trp	Gln	Ala	Gln	Ala	Val	Pro	Thr	Ile	Leu	Pro	Leu	Gly
			20						25					30

Leu	Ala	Pro	Asp	Thr	Phe	Asp	Asp	Thr	Tyr	Val	Gly	Cys	Ala	Glu
			35						40					45

Glu	Met	Glu	Glu	Lys	Ala	Ala	Pro	Leu	Leu	Lys	Glu	Glu	Met	Ala
				50					55					60

His	His	Ala	Leu	Leu	Arg	Glu	Ser	Trp	Glu	Ala	Ala	Gln	Glu	Thr
			65						70					75

Trp	Glu	Asp	Lys	Arg	Arg	Gly	Leu	Thr	Leu	Pro	Pro	Gly	Phe	Lys
			80						85					90

Ala	Gln	Asn	Gly	Ile	Ala	Ile	Met	Val	Tyr	Thr	Asn	Ser	Ser	Asn
			95						100					105

Thr	Leu	Tyr	Trp	Glu	Leu	Asn	Gln	Ala	Val	Arg	Thr	Gly	Gly	Gly
			110						115					120

Ser	Arg	Glu	Leu	Tyr	Met	Arg	His	Phe	Pro	Phe	Lys	Ala	Leu	His
			125						130					135

Phe	Tyr	Leu	Ile	Arg	Ala	Leu	Gln	Leu	Leu	Arg	Gly	Ser	Gly	Gly
			140						145					150

Cys	Ser	Arg	Gly	Pro	Gly	Glu	Val	Val	Phe	Arg	Gly	Val	Gly	Ser
			155						160					165

Leu	Arg	Phe	Glu	Pro	Lys	Arg	Leu	Gly	Asp	Ser	Val	Arg	Leu	Gly
			170						175					180

Gln	Phe	Ala	Ser	Ser	Ser	Leu	Asp	Lys	Ala	Val	Ala	His	Arg	Phe
			185						190					195

Gly	Glu	Lys	Arg	Arg	Gly	Cys	Val	Ser	Ala	Pro	Gly	Val	Gln	Leu
			200						205					210

Gly	Ser	Gln	Ser	Glu	Gly	Ala	Ser	Ser	Leu	Pro	Pro	Trp	Lys	Thr
			215						220					225

Leu	Leu	Leu	Ala	Pro	Gly	Glu	Phe	Gln	Leu	Ser	Gly	Val	Gly	Pro
			230						235					240

<210> 251

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 251

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<210> 252

<211> 1076

<212> DNA

<213> Homo sapiens

<400> 252

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caacatgcct caccctcatc tatatccttt ggcagctcac agggtcagca 100

gcctctggac ccgtgaaaga gctggtcggt tccgttggtg gggccgtgac 150

tttccccctg aagtccaaag taaagcaagt tgactctatt gtctggacct 200

tcaacacaaac ccctcttgct accatacagc cagaaggggg cactatcata 250

gtgacccaaa atcgtaatag ggagagagta gacttcccag atggaggcta 300

ctccctgaag ctacgcaaac tgaagaagaa tgactcaggg atctactatg 350

tggggatata cagctcatca ctccagcagc cctccacca ggagtacgtg 400

ctgcatgtct acgagcacct gtcaaagcct aaagtcacca tgggtctgca 450

gagcaataag aatggcacct gtgtgaccaa tctgacatgc tgcattggaac 500

atggggaaga ggatgtgatt tatacctgga aggcctggg gcaagcagcc 550

aatgagtccc ataatgggtc catcctcccc atctcctgga gatggggaga 600

aagtgatatg accttcatct gcgttgccag gaaccctgtc agcagaaaact 650

tctcaagccc catccttgcc aggaagctct gtgaagggtc tgctgatgac 700

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cagtctcttt gtactggggc tatttctttg gtttctgaag agagagagac 800

aagaagagta cattgaagag aagaagagag tggacatttg tcgggaaact 850

cctaacatat gccccattc tggagagaac acagagtacg acacaatccc 900

tcacactaat agaacaatcc taaaggaaga tccagcaaact acggtttact 950

ccactgtgga aataccgaaa aagatggaaa atccccactc actgctcacg 1000

atgccagaca caccaaggct atttgcctat gagaatgtta tctagacagc 1050

agtgactcc cctaagtctc tgctca 1076

<210> 253

<211> 335

<212> PRT

<213> Homo sapiens

<400> 253

Met Ala Gly Ser Pro Thr Cys Leu Thr Leu Ile Tyr Ile Leu Trp

1	5	10	15
Gln Leu Thr Gly Ser	Ala Ala Ser Gly	Pro Val Lys Glu Leu Val	
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Gly Ser Val Gly Gly	Ala Val Thr Phe	Pro Leu Lys Ser Lys Val	
	35	40	45
Lys Gln Val Asp Ser	Ile Val Trp Thr	Phe Asn Thr Thr Pro Leu	
	50	55	60
Val Thr Ile Gln Pro	Glu Gly Gly Thr	Ile Ile Val Thr Gln Asn	
	65	70	75
Arg Asn Arg Glu Arg	Val Asp Phe Pro	Asp Gly Gly Tyr Ser Leu	
	80	85	90
Lys Leu Ser Lys Leu	Lys Lys Asn Asp	Ser Gly Ile Tyr Tyr Val	
	95	100	105
Gly Ile Tyr Ser Ser	Ser Leu Gln Gln	Pro Ser Thr Gln Glu Tyr	
	110	115	120
Val Leu His Val Tyr	Glu His Leu Ser	Lys Pro Lys Val Thr Met	
	125	130	135
Gly Leu Gln Ser Asn	Lys Asn Gly Thr	Cys Val Thr Asn Leu Thr	
	140	145	150
Cys Cys Met Glu His	Gly Glu Glu Asp	Val Ile Tyr Thr Trp Lys	
	155	160	165
Ala Leu Gly Gln Ala	Ala Asn Glu Ser	His Asn Gly Ser Ile Leu	
	170	175	180
Pro Ile Ser Trp Arg	Trp Gly Glu Ser	Asp Met Thr Phe Ile Cys	
	185	190	195
Val Ala Arg Asn Pro	Val Ser Arg Asn	Phe Ser Ser Pro Ile Leu	
	200	205	210
Ala Arg Lys Leu Cys	Glu Gly Ala Ala	Asp Asp Pro Asp Ser Ser	
	215	220	225
Met Val Leu Leu Cys	Leu Leu Leu Val	Pro Leu Leu Leu Ser Leu	
	230	235	240
Phe Val Leu Gly Leu	Phe Leu Trp Phe	Leu Lys Arg Glu Arg Gln	
	245	250	255
Glu Glu Tyr Ile Glu	Glu Lys Lys Arg	Val Asp Ile Cys Arg Glu	
	260	265	270
Thr Pro Asn Ile Cys	Pro His Ser Gly	Glu Asn Thr Glu Tyr Asp	
	275	280	285
Thr Ile Pro His Thr	Asn Arg Thr Ile	Leu Lys Glu Asp Pro Ala	
	290	295	300
Asn Thr Val Tyr Ser	Thr Val Glu Ile	Pro Lys Lys Met Glu Asn	
	305	310	315
Pro His Ser Leu Leu	Thr Met Pro Asp	Thr Pro Arg Leu Phe Ala	

320 325 330

Tyr Glu Asn Val Ile  
335

<210> 254  
<211> 1053  
<212> DNA  
<213> Homo sapiens

<400> 254  
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ggccgtgact ttccccctga agtccaaagt aaagcaagtt gactctattg 150  
tctggacctt caacacaacc cctcttgtca ccatacagcc agaagggggc 200  
actatcatag tgacccaaaa tcgtaatagg gagagagtag acttcccaga 250  
tggaggctac tccctgaagc tcagcaaact gaagaagaat gactcaggga 300  
tctactatgt ggggatatac agctcatcac tccagcagcc ctccaccag 350  
gagtacgtgc tgcattgtcta cgagcacctg tcaaagccta aagtcaccat 400  
gggtctgcag agcaataaga atggcacctg tgtgaccaat ctgacatgct 450  
gcatggaaca tggggaagag gatgtgattt atacctggaa ggccctgggg 500  
caagcagcca atgagtccca taatgggtcc atcctcccca tctcctggag 550  
atggggagaa agtgatatga ccttcatctg cgttgccagg aaccctgtca 600  
gcagaaaactt ctcaagcccc atccttgcca ggaagctctg tgaagggtgct 650  
gctgatgacc cagattcctc catgggtcctc ctgtgtctcc tgttggtgcc 700  
cctcctgctc agtctctttg tactggggct atttctttgg tttctgaaga 750  
gagagagaca agaagagtag attgaagaga agaagagagt ggacatttgt 800  
cgggaaactc ctaacatatg cccccattct ggagagaaca cagagtacga 850  
cacaatccct cacactaata gaacaatcct aaaggaagat ccagcaaata 900  
cggtttactc cactgtggaa ataccgaaaa agatggaaaa tccccactca 950  
ctgctcacga tgccagacac accaaggcta ttgcctatg agaatgttat 1000  
ctagacagca gtgcactccc ctaagtctct gctcaaaaaa aaaaaaaaaa 1050  
aaa 1053

<210> 255  
<211> 860  
<212> DNA  
<213> Homo sapiens

<400> 255  
gaaagacgtg gtcttgacag acagacaatc ctattcccta ccaaaatgaa 50

gatgctgctg ctgctgtgtt tgggactgac cctagtctgt gtccatgcag 100  
 aagaagctag ttctacggga aggaacttta atgtagaaaa gattaatggg 150  
 gaatggcata ctattatcct ggcctctgac aaaagagaaa agatagaaga 200  
 acatggcaac tttagacttt ttctggagca aatccatgtc ttggagaatt 250  
 ccttagttct taaagtccat actgtaagag atgaagagtg ctccgaatta 300  
 tctatgggtg ctgacaaaac agaaaaggct ggtgaatatt ctgtgacgta 350  
 tgatggattc aatacattta ctatacctaa gacagactat gataactttc 400  
 ttatggctca cctcattaac gaaaaggatg gggaaacott ccagctgatg 450  
 gggctctatg gccgagaacc agatttgagt tcagacatca aggaaagggt 500  
 tgcacaacta tgtgaggagc atggaatcct tagagaaaat atcattgacc 550  
 tatccaatgc caatcgctgc ctccaggccc gagaatgaag aatggcctga 600  
 gcctccagtg ttgagtggac acttctcacc aggactccac catcatccct 650  
 tcctatccat acagcatccc cagtataaat tctgtgatct gcattccatc 700  
 ctgtctcact gagaagtcca attccagtct atcaacatgt tacctaggat 750  
 acctcatcaa gaatcaaaga cttctttaaa tttctctttg atacaccctt 800  
 gacaattttt catgaaatta ttctcttcc tgttcaataa atgattaccc 850  
 ttgcacttaa 860

<210> 256  
 <211> 180  
 <212> PRT  
 <213> Homo sapiens

<400> 256  
 Met Lys Met Leu Leu Leu Cys Leu Gly Leu Thr Leu Val Cys  
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 Val His Ala Glu Glu Ala Ser Ser Thr Gly Arg Asn Phe Asn Val  
 20 25 30  
 Glu Lys Ile Asn Gly Glu Trp His Thr Ile Ile Leu Ala Ser Asp  
 35 40 45  
 Lys Arg Glu Lys Ile Glu Glu His Gly Asn Phe Arg Leu Phe Leu  
 50 55 60  
 Glu Gln Ile His Val Leu Glu Asn Ser Leu Val Leu Lys Val His  
 65 70 75  
 Thr Val Arg Asp Glu Glu Cys Ser Glu Leu Ser Met Val Ala Asp  
 80 85 90  
 Lys Thr Glu Lys Ala Gly Glu Tyr Ser Val Thr Tyr Asp Gly Phe  
 95 100 105  
 Asn Thr Phe Thr Ile Pro Lys Thr Asp Tyr Asp Asn Phe Leu Met  
 110 115 120

Ala	His	Leu	Ile	Asn	Glu	Lys	Asp	Gly	Glu	Thr	Phe	Gln	Leu	Met
				125					130					135
Gly	Leu	Tyr	Gly	Arg	Glu	Pro	Asp	Leu	Ser	Ser	Asp	Ile	Lys	Glu
				140					145					150
Arg	Phe	Ala	Gln	Leu	Cys	Glu	Glu	His	Gly	Ile	Leu	Arg	Glu	Asn
				155					160					165
Ile	Ile	Asp	Leu	Ser	Asn	Ala	Asn	Arg	Cys	Leu	Gln	Ala	Arg	Glu
				170					175					180

<210> 257  
 <211> 766  
 <212> DNA  
 <213> Homo sapiens

<400> 257  
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 ttctcaatgc gatacctcta attgtcagct tagttgagga agaccaatth 150  
 tctcaaaacc ccatctcttg ctttgagtgg tggttcccag gaattatagg 200  
 agcaggtctg atggccattc cagcaacaac aatgtccttg acagcaagaa 250  
 aaagagcgtg ctgcaacaac agaactggaa tgtttctttc atcatttttc 300  
 agtgtgatca cagtcattgg tgctctgtat tgcattgctga tatccatcca 350  
 ggctctctta aaaggctctc tcatgtgtaa ttctccaagc aacagtaatg 400  
 ccaattgtga attttcattg aaaaacatca gtgacattca tccagaatcc 450  
 ttcaacttgc agtggttttt caatgactct tgtgcacctc ctactgggtt 500  
 caataaacc accagtaacg acaccatggc gagtggctgg agagcatcta 550  
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 cagtcagata gtcacgggtt tccttggttg tctgtgtgga gtctctaagc 700  
 gaagaagtca aattgtgtag tttaatggga ataaaatgta agtatcagta 750  
 gtttgaaaaa aaaaaa 766

<210> 258  
 <211> 229  
 <212> PRT  
 <213> Homo sapiens

<400> 258  
 Met Thr Cys Cys Glu Gly Trp Thr Ser Cys Asn Gly Phe Ser Leu  
 1 5 10 15  
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 20 25 30  
 Ile Val Ser Leu Val Glu Glu Asp Gln Phe Ser Gln Asn Pro Ile



35									40					45	
Ser	Cys	Phe	Glu	Trp 50	Trp	Phe	Pro	Gly	Ile 55	Ile	Gly	Ala	Gly	Leu 60	
Met	Ala	Ile	Pro	Ala 65	Thr	Thr	Met	Ser	Leu 70	Thr	Ala	Arg	Lys	Arg 75	
Ala	Cys	Cys	Asn	Asn 80	Arg	Thr	Gly	Met	Phe 85	Leu	Ser	Ser	Phe	Phe 90	
Ser	Val	Ile	Thr	Val 95	Ile	Gly	Ala	Leu	Tyr 100	Cys	Met	Leu	Ile	Ser 105	
Ile	Gln	Ala	Leu	Leu 110	Lys	Gly	Pro	Leu	Met 115	Cys	Asn	Ser	Pro	Ser 120	
Asn	Ser	Asn	Ala	Asn 125	Cys	Glu	Phe	Ser	Leu 130	Lys	Asn	Ile	Ser	Asp 135	
Ile	His	Pro	Glu	Ser 140	Phe	Asn	Leu	Gln	Trp 145	Phe	Phe	Asn	Asp	Ser 150	
Cys	Ala	Pro	Pro	Thr 155	Gly	Phe	Asn	Lys	Pro 160	Thr	Ser	Asn	Asp	Thr 165	
Met	Ala	Ser	Gly	Trp 170	Arg	Ala	Ser	Ser	Phe 175	His	Phe	Asp	Ser	Glu 180	
Glu	Asn	Lys	His	Arg 185	Leu	Ile	His	Phe	Ser 190	Val	Phe	Leu	Gly	Leu 195	
Leu	Leu	Val	Gly	Ile 200	Leu	Glu	Val	Leu	Phe 205	Gly	Leu	Ser	Gln	Ile 210	
Val	Ile	Gly	Phe	Leu 215	Gly	Cys	Leu	Cys	Gly 220	Val	Ser	Lys	Arg	Arg 225	
Ser	Gln	Ile	Val												

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<210> 259
<211> 434
<212> DNA
<213> Homo sapiens
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[illegible]

<210> 260

<211> 83

<212> PRT

<213> Homo sapiens

<400> 260

Met Arg Leu Ser Val Cys Leu Leu Met Val Ser Leu Ala Leu Cys  
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Cys Tyr Gln Ala His Ala Leu Val Cys Pro Ala Val Ala Ser Glu  
20 25 30

Ile Thr Val Phe Leu Phe Leu Ser Asp Ala Ala Val Asn Leu Gln  
35 40 45

Val Ala Lys Leu Asn Pro Pro Pro Glu Ala Leu Ala Ala Lys Leu  
50 55 60

Glu Val Lys His Cys Thr Asp Gln Ile Ser Phe Lys Lys Arg Leu  
65 70 75

Ser Leu Lys Lys Ser Trp Trp Lys  
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<210> 261

<211> 636

<212> DNA

<213> Homo sapiens

<400> 261

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ctgaccaatt	gagctgtgag	cctggagcag	atccgtgggc	tgcagacccc	150
cgccccagtg	cctctcccc	tgcagccctg	cccctcgaac	tgtgacatgg	200
agagagtgac	cctggccctt	ctcctactgg	caggcctgac	tgccttgga	250
gccaatgacc	catttgccaa	taaagacgat	cccttctact	atgactggaa	300
aaacctgcag	ctgagcggac	tgatctgcgg	agggtcctg	gccattgctg	350
ggatcgcggc	agttctgagt	ggcaaatgca	aatacaagag	cagccagaag	400
cagcacagtc	ctgtacctga	gaaggccatc	ccactcatca	ctccaggctc	450
tgccactact	tgctgagcac	aggactggcc	tccagggatg	gcctgaagcc	500
taacactggc	cccagcacc	tcctcccctg	ggaggcctta	tcctcaagga	550
aggactttctc	tccaagggca	ggctgttagg	cccctttctg	atcaggaggc	600
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<210> 262

<211> 89

<212> PRT

<213> Homo sapiens

[illegible]

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<210> 263
<211> 1676
<212> DNA
<213> Homo sapiens
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ggacctatgc	cttctataac	aactgccgcc	ggctccagtg	tttcccacag	200
cccccaaac	ggaactgggt	ttgggggtcac	ctgggcctga	tcactcctac	250
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gctttacggg	atggctgggt	cccatcatcc	ccttcacgt	tttatgccac	350
cctgacacca	tccggtctat	caccaatgcc	tcagctgcc	ttgcaccaa	400
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gccttccatt	tcaacatcct	gaagtcctat	ataacgatct	tcaacaagag	550
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gtcgtctgga	catgtttgag	cacatcagcc	tcacgacctt	ggacagtcta	650
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ctgagcaagg atgaagatgg gaaggcattg tcagatgagg atataagagc 1000  
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 tctcctgggt cctgtacaac cttgcgaggc acccagaata ccaggagcgc 1100  
 tgccgacagg aggtgcaaga gcttctgaag gaccgcatc ctaaagagat 1150  
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 agagcctgag gttacatccc ccagctccct tcctctcccg atgctgcacc 1250  
 caggacattg ttctcccaga tggccgagtc atccccaaag gcattacctg 1300  
 cctcatogat attatagggg tccatcacia cccaactgtg tggccggatc 1350  
 ctgaggtcta cgacccttc cgctttgacc cagagaacag caaggggagg 1400  
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 gtcatgaata aaacggtgct gtcaaa 1676

<210> 264  
 <211> 524  
 <212> PRT  
 <213> Homo sapiens

<400> 264  
 Met Ser Leu Leu Ser Leu Pro Trp Leu Gly Leu Arg Pro Val Ala  
 1 5 10 15  
 Met Ser Pro Trp Leu Leu Leu Leu Val Val Gly Ser Trp Leu  
 20 25 30  
 Leu Ala Arg Ile Leu Ala Trp Thr Tyr Ala Phe Tyr Asn Asn Cys  
 35 40 45  
 Arg Arg Leu Gln Cys Phe Pro Gln Pro Pro Lys Arg Asn Trp Phe  
 50 55 60  
 Trp Gly His Leu Gly Leu Ile Thr Pro Thr Glu Glu Gly Leu Lys  
 65 70 75  
 Asp Ser Thr Gln Met Ser Ala Thr Tyr Ser Gln Gly Phe Thr Val  
 80 85 90  
 Trp Leu Gly Pro Ile Ile Pro Phe Ile Val Leu Cys His Pro Asp  
 95 100 105  
 Thr Ile Arg Ser Ile Thr Asn Ala Ser Ala Ala Ile Ala Pro Lys  
 110 115 120  
 Asp Asn Leu Phe Ile Arg Phe Leu Lys Pro Trp Leu Gly Glu Gly  
 125 130 135

Ile	Leu	Leu	Ser	Gly	Gly	Asp	Lys	Trp	Ser	Arg	His	Arg	Arg	Met	
				140					145					150	
Leu	Thr	Pro	Ala	Phe	His	Phe	Asn	Ile	Leu	Lys	Ser	Tyr	Ile	Thr	
				155					160					165	
Ile	Phe	Asn	Lys	Ser	Ala	Asn	Ile	Met	Leu	Asp	Lys	Trp	Gln	His	
				170					175					180	
Leu	Ala	Ser	Glu	Gly	Ser	Ser	Arg	Leu	Asp	Met	Phe	Glu	His	Ile	
				185					190					195	
Ser	Leu	Met	Thr	Leu	Asp	Ser	Leu	Gln	Lys	Cys	Ile	Phe	Ser	Phe	
				200					205					210	
Asp	Ser	His	Cys	Gln	Glu	Arg	Pro	Ser	Glu	Tyr	Ile	Ala	Thr	Ile	
				215					220					225	
Leu	Glu	Leu	Ser	Ala	Leu	Val	Glu	Lys	Arg	Ser	Gln	His	Ile	Leu	
				230					235					240	
Gln	His	Met	Asp	Phe	Leu	Tyr	Tyr	Leu	Ser	His	Asp	Gly	Arg	Arg	
				245					250					255	
Phe	His	Arg	Ala	Cys	Arg	Leu	Val	His	Asp	Phe	Thr	Asp	Ala	Val	
				260					265					270	
Ile	Arg	Glu	Arg	Arg	Arg	Thr	Leu	Pro	Thr	Gln	Gly	Ile	Asp	Asp	
				275					280					285	
Phe	Phe	Lys	Asp	Lys	Ala	Lys	Ser	Lys	Thr	Leu	Asp	Phe	Ile	Asp	
				290					295					300	
Val	Leu	Leu	Leu	Ser	Lys	Asp	Glu	Asp	Gly	Lys	Ala	Leu	Ser	Asp	
				305					310					315	
Glu	Asp	Ile	Arg	Ala	Glu	Ala	Asp	Thr	Phe	Met	Phe	Gly	Gly	His	
				320					325					330	
Asp	Thr	Thr	Ala	Ser	Gly	Leu	Ser	Trp	Val	Leu	Tyr	Asn	Leu	Ala	
				335					340					345	
Arg	His	Pro	Glu	Tyr	Gln	Glu	Arg	Cys	Arg	Gln	Glu	Val	Gln	Glu	
				350					355					360	
Leu	Leu	Lys	Asp	Arg	Asp	Pro	Lys	Glu	Ile	Glu	Trp	Asp	Asp	Leu	
				365					370					375	
Ala	Gln	Leu	Pro	Phe	Leu	Thr	Met	Cys	Val	Lys	Glu	Ser	Leu	Arg	
				380					385					390	
Leu	His	Pro	Pro	Ala	Pro	Phe	Ile	Ser	Arg	Cys	Cys	Thr	Gln	Asp	
				395					400					405	
Ile	Val	Leu	Pro	Asp	Gly	Arg	Val	Ile	Pro	Lys	Gly	Ile	Thr	Cys	
				410					415					420	
Leu	Ile	Asp	Ile	Ile	Gly	Val	His	His	Asn	Pro	Thr	Val	Trp	Pro	
				425					430					435	
Asp	Pro	Glu	Val	Tyr	Asp	Pro	Phe	Arg	Phe	Asp	Pro	Glu	Asn	Ser	
				440					445					450	

Lys Gly Arg Ser Pro Leu Ala Phe Ile Pro Phe Ser Ala Gly Pro  
455 460 465

Arg Asn Cys Ile Gly Gln Ala Phe Ala Met Ala Glu Met Lys Val  
470 475 480

Val Leu Ala Leu Met Leu Leu His Phe Arg Phe Leu Pro Asp His  
485 490 495

Thr Glu Pro Arg Arg Lys Leu Glu Leu Ile Met Arg Ala Glu Gly  
500 505 510

Gly Leu Trp Leu Arg Val Glu Pro Leu Asn Val Gly Leu Gln  
515 520

<210> 265  
<211> 584  
<212> DNA  
<213> Homo sapiens

<400> 265  
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tcttcctctc cttgactcca gggaaatata ctttcaactc tcagcacctc 150  
atgaagacgc gcgcttaact ccggaggagc tagaaagagc ttcccttcta 200  
cagatattgc cagagatgct ggggtgcagaa agaggggata ttctcaggaa 250  
agcagactca agtaccaaca tttttaaccc aagaggaaat ttgagaaagt 300  
ttcaggattt ctctggacaa gatcctaaca ttttactgag tcattctttg 350  
gccagaatct ggaaaccata caagaaacgt gagactcctg attgcttctg 400  
gaaatactgt gtctgaagtg aaataagcat ctgttagtca gctcagaaac 450  
acccatctta gaatatgaaa aataacacaa tgcttgattt gaaaacagtg 500  
tggagaaaaa ctaggcaaac tacaccctgt tcattgttac ctggaaaata 550  
aatcctctat gttttgcaca aaaaaaaaaa aaaa 584

<210> 266  
<211> 124  
<212> PRT  
<213> Homo sapiens

<400> 266  
Met Tyr Lys Leu Ala Ser Cys Cys Leu Leu Phe Thr Gly Phe Leu  
1 5 10 15  
Asn Pro Leu Leu Ser Leu Pro Leu Leu Asp Ser Arg Glu Ile Ser  
20 25 30  
Phe Gln Leu Ser Ala Pro His Glu Asp Ala Arg Leu Thr Pro Glu  
35 40 45  
Glu Leu Glu Arg Ala Ser Leu Leu Gln Ile Leu Pro Glu Met Leu  
50 55 60

Gly Ala Glu Arg Gly Asp Ile Leu Arg Lys Ala Asp Ser Ser Thr  
65 70 75  
Asn Ile Phe Asn Pro Arg Gly Asn Leu Arg Lys Phe Gln Asp Phe  
80 85 90  
Ser Gly Gln Asp Pro Asn Ile Leu Leu Ser His Leu Leu Ala Arg  
95 100 105  
Ile Trp Lys Pro Tyr Lys Lys Arg Glu Thr Pro Asp Cys Phe Trp  
110 115 120  
Lys Tyr Cys Val

<210> 267  
<211> 654  
<212> DNA  
<213> Homo sapiens

<400> 267  
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cacctctggg atgggggttg tggtttaaaa caaacgccag tcatcctata 100  
taaggacctg acagccacca ggcaccacct ccgccaggaa ctgcaggccc 150  
acctgtctgc aaccacagctg aggccatgcc ctccccaggg accgtctgca 200  
gcctcctgct cctcggcatg ctctggctgg acttggccat ggcaggctcc 250  
agcttctcta gccctgaaca ccagagagtc cagcagagaa aggagtcgaa 300  
gaagccacca gccaagctgc agccccgagc tctagcaggc tggctccgcc 350  
cggaagatgg aggtcaagca gaagggggcag aggatgaact ggaagtccgg 400  
ttcaacgccc cttttgatgt tggaatcaag ctgtcagggg ttcagtacca 450  
gcagcacagc caggccctgg ggaagtttct tcaggacatc ctctgggaag 500  
aggccaaaga ggccccagcc gacaagtgat cgcccacaag ctttactcac 550  
ctctctctaa gtttagaagc gctcatctgg cttttcgctt gcttctgcag 600  
caactcccac gactgttgta caagctcagg aggcgaataa atgttcaaac 650  
tgta 654

<210> 268  
<211> 117  
<212> PRT  
<213> Homo sapiens

<400> 268  
Met Pro Ser Pro Gly Thr Val Cys Ser Leu Leu Leu Leu Gly Met  
1 5 10 15  
Leu Trp Leu Asp Leu Ala Met Ala Gly Ser Ser Phe Leu Ser Pro  
20 25 30  
Glu His Gln Arg Val Gln Gln Arg Lys Glu Ser Lys Lys Pro Pro  
35 40 45

Ala	Lys	Leu	Gln	Pro	Arg	Ala	Leu	Ala	Gly	Trp	Leu	Arg	Pro	Glu
				50					55					60
Asp	Gly	Gly	Gln	Ala	Glu	Gly	Ala	Glu	Asp	Glu	Leu	Glu	Val	Arg
				65					70					75
Phe	Asn	Ala	Pro	Phe	Asp	Val	Gly	Ile	Lys	Leu	Ser	Gly	Val	Gln
				80					85					90
Tyr	Gln	Gln	His	Ser	Gln	Ala	Leu	Gly	Lys	Phe	Leu	Gln	Asp	Ile
				95					100					105
Leu	Trp	Glu	Glu	Ala	Lys	Glu	Ala	Pro	Ala	Asp	Lys			
				110					115					

<210> 269  
 <211> 1332  
 <212> DNA  
 <213> Homo sapiens

<400> 269  
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 gtccagtacc tcgtgaaccc cggggtgctc cgcacggacc ccagatgtca 100  
 agaatatgaa cacgtggctg ctgttcctcc ccctgttccc ggtgcagggtg 150  
 cagaccctga tagtcgtgat catcgggatg ctcgtgctcc tgctggactt 200  
 tcttggcttg gtgcacctgg gccagctgct catcttcac atctacctga 250  
 gtatgtcccc caccctaagc cccgatccc cccaaggctg ggtggtcaga 300  
 gctgctcatc ttacacctct acttgagtat gtccctaacc ctgagcccc 350  
 cacgcctggg gccagagtct ttgtcccccg tgtgcgcatg tgttcagggt 400  
 cagcctctcc cagaagttag atcatggaca aaaagggcaa atcacaggaa 450  
 gaaattaaat ccatgaggac ccagcaggcc cagcaagaag ctgaactcac 500  
 gccgagacct gcaggagtgg tgccagggtc ttgaagtaac aagtttaaaa 550  
 tgttcagaga caatggaatg gaatctatta ggcaagaaca ggacattatg 600  
 aaataaggac aggtggactt caaaaaacac aagtagaat tctaacaatg 650  
 aaatatatta caggcaggtc acccactaac caaacaactg aagcgagagc 700  
 tgtggtcttg cttggtctca cagtgggcac agcggtaggc ggtcagtcac 750  
 gttgctgaac gacggagggt aaactcccca gcccagaagaa aacctgtgtt 800  
 ggaagtaaca acaacctccc tgctcctggc accagccgtt ttggtcatgg 850  
 tgggccagct gcaaagcgtc ttccattctc tgggcagtgg tggccccgag 900  
 gctgtggcct ctcaggggtt ttctgtggac acgggcagca gagtgtgtcc 950  
 aggccagccc ccaagaatgc cctgtcctg acagcttggc caaccctgg 1000  
 tcagggcaga gggagtggg tgggtcaggc tctgggctca cctccatctc 1050







	35	40	45
Pro Lys Pro Leu Cys Glu Lys Gly Leu Ala Ala Lys Cys Phe Asp	50	55	60
Met Pro Val Ser Leu Asp Gly Asp Thr Asn Thr Ser Thr Gln Glu	65	70	75
Val Val Gln Tyr Asn Trp Glu Thr Gly Asp Asp Arg Phe Ser Phe	80	85	90
Arg Ser Phe Arg Ser Gly Met Trp Leu Ser Cys Glu Glu Thr Val	95	100	105
Glu Glu Pro Gly Glu Arg Cys Arg Ser Phe Ile Glu Leu Thr Pro	110	115	120
Pro Ala Lys Arg Gly Glu Lys Gly Leu Leu Glu Phe Ala Thr Leu	125	130	135
Gln Gly Pro Cys His Pro Thr Leu Arg Phe Gly Gly Lys Arg Leu	140	145	150
Met Glu Lys Ala Ser Leu Pro Ser Pro Pro Leu Gly Leu Cys Gly	155	160	165
Lys Asn Pro Met Val Ile Pro Gly Asn Ala Asp His Leu His Arg	170	175	180
Thr Ser Ile His Gln Leu Pro Pro Ala Thr Asn Arg Leu Ala Thr	185	190	195
His Trp Glu Pro Cys Leu Trp Ala Gln Thr Glu Arg Leu Cys Cys	200	205	210
Cys Phe Leu Cys Pro Val Arg Ser Pro Gly Asp Gly Gly Pro His	215	220	225
Asp Val Phe Thr Ser Leu Pro Ser Asp Cys Gln Leu Gly Ser Arg	230	235	240
Arg Leu Glu Thr Thr Cys Leu Glu Leu Trp Leu Gly Leu Leu His	245	250	255
Gly Leu Ala Leu Leu His Leu Leu His Gly Val Gly Cys His His	260	265	270
Leu Gln His Val His Gln Asp Gly Ala Gly Val Gln Val Gln Ala	275	280	285

<210> 273

<211> 1158

<212> DNA

<213> Homo sapiens

<400> 273

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 ctcacttaag tctcaggcct gtcagcagct cctgtggaca ttgccatccc 150  
 ctctggtagc cttcagagca aacaggacaa cctatgttat ggatgtttcc 200

accaaccagg gtagtggcat ggagcaccgt aaccatctgt gcttctgtga 250  
 tcttatgac agagccactt ctccacctct gaaatgttcc ctgctctgaa 300  
 atctggcatg agatggcaca ggtgaccacg cagaagccac cagaatcttg 350  
 cctgccctat tctctctccc aagtctgttc tcttattgtc aacctcagca 400  
 caacaggctg ggcgaatgg cttacagag aaagcaatct gtgtggctag 450  
 tgggcagatt accatgcaag cccagagaga aatggaggag cttttagacc 500  
 acctccctgt cagccagtat taacatgtcc ccttccccct gccccgccgt 550  
 agattcagga cattogcccc tgtgtgccac caaaccagga ctttccccct 600  
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 gggcagtgtg gcatctttca agctccgtta ctatggcgat ggccatgatg 700  
 ttacaatccc acttgcctga ataataaagt gggaagggga agcagaggga 750  
 aatggggcca tgtgaatgca gctgctctgt tctccctacc ctgaggaaaa 800  
 accaaagggga agcaacagga acttctgcaa ctgggttttta tcgaaagat 850  
 catcctgcct gcagatgctg ttgaaggggc acaagaaatg tagctggaga 900  
 agattgatga aagtgcaggt gtgtaaggaa atagaacagt ctgctgggag 950  
 tcagacctgg aattctgatt ccaaactctt tattactttg ggaagtcact 1000  
 cagcctcccc gtagccatct ccagggtgac ggaacccagt gtattacctg 1050  
 ctggaaccaa ggaaactaac aatgtaggtt actagtgaat accccaatgg 1100  
 tttctccaat tatgcccatg ccacaaaac aataaaacaa aattctctaa 1150  
 cactgaaa 1158

<210> 274  
 <211> 86  
 <212> PRT  
 <213> Homo sapiens

<400> 274  
 Met Trp Leu Pro Leu Gly Leu Leu Ser Leu Cys Leu Ser Pro Leu  
 1 5 10 15  
 Pro Ile Leu Ser Ser Pro Ser Leu Lys Ser Gln Ala Cys Gln Gln  
 20 25 30  
 Leu Leu Trp Thr Leu Pro Ser Pro Leu Val Ala Phe Arg Ala Asn  
 35 40 45  
 Arg Thr Thr Tyr Val Met Asp Val Ser Thr Asn Gln Gly Ser Gly  
 50 55 60  
 Met Glu His Arg Asn His Leu Cys Phe Cys Asp Leu Tyr Asp Arg  
 65 70 75  
 Ala Thr Ser Pro Pro Leu Lys Cys Ser Leu Leu  
 80 85

<210> 275  
 <211> 2694  
 <212> DNA  
 <213> Homo sapiens

<400> 275  
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 gtcgtggagc caggagcgac gtcaccgccca tggcaggcat caaagctttg 100  
 attagtgttg cctttggagg agcaatcgga ctgatgtttt tgatgcttgg 150  
 atgtgccctt ccaatataca acaaatactg gccctctttt gttctatttt 200  
 ttacatcctt ttcacctatt ccatactgca tagcaagaag attagtggat 250  
 gatacagatg ctatgagtaa cgcttgtaag gaacttgcca tctttcttac 300  
 aacgggcatt gtcgtgtcag cttttggact ccctattgta tttgccagag 350  
 cacatctgat tgagtgggga gcttgtgcac ttgttctcac aggaaacaca 400  
 gtcactcttg caactatact aggctttttc ttgggtcttg gaagcaatga 450  
 cgacttcagc tggcagcagt ggtgaaaaga aattactgaa ctattgtcaa 500  
 atggacttcc tgtcatttgt tggccattca cgcacacagg agatggggca 550  
 gttaatgctg aatggtatag caagcctctt ggggggtatt taggtgctcc 600  
 cttctcactt ttattgtaag catactattt tcacagagac ttgctgaagg 650  
 attaaaagga ttttctcttt tggaaaagct tgactgattt cacacttatt 700  
 tatagtatgc tttttgtggt gtctgtctga atttaaatat ttatgtgttt 750  
 ttctgttag gttgattttt tttggaatca atatgcaatg ttaaactatt 800  
 ttttaatgta atcatttgca ttggttagga attcagaatt ccgccggctc 850  
 tattactggt caagtacatc ttttctctta aaattattta gcctccatta 900  
 ttacaaaaaa ttataaaaat aagttttcag tcagtcagga tgacatcact 950  
 cccaatgtta tgcagacata cagacggttg gcatacgtta tagactgtat 1000  
 actcagtgc aatatagctg cttttatacc tcagaggggc caagtgttaa 1050  
 tgcccatgcc ctccgttaag ggttgttggg tttactggta gacagatgtt 1100  
 ttgtggattg aaaattatth tatggaattg ctacagagga gtgcttttct 1150  
 tctcaattgt tagaagaatt tatgttaaag ttttaaggtaa ggggtgtaaa 1200  
 acatttttga gataagggtt ttatttatgt ttattattgt tagagtgagt 1250  
 tgcaatgtgg gaagaaatga cattgaaatt ccagtttttg aatcctgttt 1300  
 ctatttataa gtgaaatttg tgatctccta tcaacctttc atgttttacc 1350  
 ctgttaaaat ggacatacat ggaaccaata ctgatgaggg acagttgtat 1400  
 gtttgcatca tatatgccag aaaaccttcc tctgcttctt ccttttgact 1450

tatttgggtat gttgtatata ttacataaaa taacttttca aatatagttt 1500  
aataacactt agaagtgttt acttacctgg aaaataattg ctatgccgta 1550  
cattcagagt gccccctccc ctgcaaggcc ttgccatgat taacaagtaa 1600  
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gagttaatgc aaagtagcca agtccagcta tatagcagct tcagaaacat 1850  
acctgaccaa aaaattccca gtaaccaggc atgatcaatt tatagtggtc 1900  
gtttacatct aataattatc aggacttttt tcaggagtgg gttataaaaa 1950  
cattcaagtt ggtctgacag tattttgtta aggatatttg tttgtatgtt 2000  
tattcagtat acttacataa aaattatttc gccatcagcc aaaactcagt 2050  
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ggaataaatt tgggatttgt tcagcttttt tactaaagat gcctaaagcc 2150  
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ggaagcagga cgaaatatcg gcgtgtggct ggagccttcc cactggaggc 2250  
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ggtacacatg agttagagag ctggtgagac agttgggaac tctttgtgct 2350  
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cctattttct gttctggatg tcagtgcagt gcactgctac tgttttatcc 2450  
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ttgcattggc agcattgtgt ctttgacctt gtatactagc ttgacatagt 2550  
gctgtctctg atttctaggc tagttacttg agatatgaat tttccataga 2600  
atatgcactg atacaacatt accattcttc tatggaaaga aaacttttga 2650  
tgatgaaaca ataaagattt taaatatcta ttttaaaaaa aaaa 2694

<210> 276

<211> 131

<212> PRT

<213> Homo sapiens

<400> 276

Met Ala Gly Ile Lys Ala Leu Ile Ser Leu Ser Phe Gly Gly Ala  
1 5 10 15

Ile Gly Leu Met Phe Leu Met Leu Gly Cys Ala Leu Pro Ile Tyr  
20 25 30

Asn Lys Tyr Trp Pro Leu Phe Val Leu Phe Phe Tyr Ile Leu Ser

	35		40		45
Pro Ile Pro Tyr Cys Ile Ala Arg Arg Leu Val Asp Asp Thr Asp	50		55		60
Ala Met Ser Asn Ala Cys Lys Glu Leu Ala Ile Phe Leu Thr Thr	65		70		75
Gly Ile Val Val Ser Ala Phe Gly Leu Pro Ile Val Phe Ala Arg	80		85		90
Ala His Leu Ile Glu Trp Gly Ala Cys Ala Leu Val Leu Thr Gly	95		100		105
Asn Thr Val Ile Phe Ala Thr Ile Leu Gly Phe Phe Leu Val Phe	110		115		120
Gly Ser Asn Asp Asp Phe Ser Trp Gln Gln Trp	125		130		

<210> 277  
 <211> 4104  
 <212> DNA  
 <213> Homo sapiens

<400> 277  
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 cacactgcct ggtggaggga aggagcccg ggcctctctg ccgctccccg 150  
 cgccgcgcgtc cgcaacctcc caccgcccgc cgcccgccgc ccgcccgcgc 200  
 caaagcatga gtgagccgcg tctctgcagc tgcccggggc gcgaatggca 250  
 ggctgtttcc goggagtaaa aggtggcgcc ggtcagtggc cgtttccaat 300  
 gacggacatt aaccagactg tcagatcctg gggagtcgcg agccccgagt 350  
 ttggagtttt ttccccccac aacgtcacag tccgaactgc agagggaaag 400  
 gaaggcgcca ggaaggcgaa gctcgggctc cggcacgtag ttgggaaact 450  
 tgccgggtcct agaagtcgcc tccccgcctt gccggccgcc cttgcagccc 500  
 cgagccgagc agcaaagtga gacattgtgc gctgccaga tccgccggcc 550  
 gcggaccggg gctgcctcgg aaacacagag ggtctttctc tcgccctgca 600  
 tataattagc ctgcacacaa agggagcagc tgaatggagg ttgtcactct 650  
 ctggaaaagg atttctgacc gagcgcttcc aatggacatt ctccagtctc 700  
 tctggaaaga ttctcgctaa tggatttcct gctgctcggc ctctgtctat 750  
 actggctgct gaggaggccc tcgggggtgg tcttgtgtct gctggggggc 800  
 tgctttcaga tgctgccgcg cgccccagc gggtgccgcg agctgtgccg 850  
 gtgcgagggg cggctgctgt actgcgagc gctcaacctc accgagggcg 900  
 ccacaaacct gtccggcctg ctgggcttgt ccctgcgcta caacagcctc 950

tcggagctgc gcgccggcca gttcacgggg ttaatgcagc tcacgtggct 1000  
ctatctggat cacaatcaca totgtccgt gcagggggac gcctttcaga 1050  
aactgcgccg agttaaggaa ctacgctga gttccaacca gatcacccaa 1100  
ctgcccaca ccaccttcg gccatgccc aacctgcgca gcgtggacct 1150  
ctcgtacaac aagctgcagg cgctcgcgcc cgacctcttc cacgggctgc 1200  
ggaagctcac cacgctgcat atgcgggcca acgcatcca gtttgtgccc 1250  
gtgcgcatct tccaggactg ccgcagcctc aagtttctcg acatcggata 1300  
caatcagctc aagagtctgg cgcgcaactc tttcgccggc ttgtttaagc 1350  
tcaccgagct gcacctcgag cacaacgact tggtaagggt gaacttcgcc 1400  
cacttcccgc gcctcatctc cctgcactcg ctctgcctgc ggaggaacaa 1450  
ggtggccatt gtggtcagct cgctggactg ggtttggaac ctggagaaaa 1500  
tggacttgtc gggcaacgag atcgagtaca tggagcccca tgtgttcgag 1550  
accgtgccgc acctgcagtc cctgcagctg gactccaacc gcctcaccta 1600  
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<210> 278  
 <211> 522  
 <212> PRT  
 <213> Homo sapiens

<400> 278

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Arg	Pro	Ser	Gly	Val	Val	Leu	Cys	Leu	Leu	Gly	Ala	Cys	Phe	Gln
				20					25					30
Met	Leu	Pro	Ala	Ala	Pro	Ser	Gly	Cys	Pro	Gln	Leu	Cys	Arg	Cys
				35					40					45
Glu	Gly	Arg	Leu	Leu	Tyr	Cys	Glu	Ala	Leu	Asn	Leu	Thr	Glu	Ala
				50					55					60
Pro	His	Asn	Leu	Ser	Gly	Leu	Leu	Gly	Leu	Ser	Leu	Arg	Tyr	Asn
				65					70					75
Ser	Leu	Ser	Glu	Leu	Arg	Ala	Gly	Gln	Phe	Thr	Gly	Leu	Met	Gln
				80					85					90
Leu	Thr	Trp	Leu	Tyr	Leu	Asp	His	Asn	His	Ile	Cys	Ser	Val	Gln
				95					100					105
Gly	Asp	Ala	Phe	Gln	Lys	Leu	Arg	Arg	Val	Lys	Glu	Leu	Thr	Leu
				110					115					120
Ser	Ser	Asn	Gln	Ile	Thr	Gln	Leu	Pro	Asn	Thr	Thr	Phe	Arg	Pro
				125					130					135
Met	Pro	Asn	Leu	Arg	Ser	Val	Asp	Leu	Ser	Tyr	Asn	Lys	Leu	Gln
				140					145					150
Ala	Leu	Ala	Pro	Asp	Leu	Phe	His	Gly	Leu	Arg	Lys	Leu	Thr	Thr
				155					160					165
Leu	His	Met	Arg	Ala	Asn	Ala	Ile	Gln	Phe	Val	Pro	Val	Arg	Ile
				170					175					180
Phe	Gln	Asp	Cys	Arg	Ser	Leu	Lys	Phe	Leu	Asp	Ile	Gly	Tyr	Asn
				185					190					195
Gln	Leu	Lys	Ser	Leu	Ala	Arg	Asn	Ser	Phe	Ala	Gly	Leu	Phe	Lys
				200					205					210
Leu	Thr	Glu	Leu	His	Leu	Glu	His	Asn	Asp	Leu	Val	Lys	Val	Asn
				215					220					225
Phe	Ala	His	Phe	Pro	Arg	Leu	Ile	Ser	Leu	His	Ser	Leu	Cys	Leu
				230					235					240
Arg	Arg	Asn	Lys	Val	Ala	Ile	Val	Val	Ser	Ser	Leu	Asp	Trp	Val
				245					250					255
Trp	Asn	Leu	Glu	Lys	Met	Asp	Leu	Ser	Gly	Asn	Glu	Ile	Glu	Tyr
				260					265					270
Met	Glu	Pro	His	Val	Phe	Glu	Thr	Val	Pro	His	Leu	Gln	Ser	Leu
				275					280					285

Gln	Leu	Asp	Ser	Asn	Arg	Leu	Thr	Tyr	Ile	Glu	Pro	Arg	Ile	Leu	
				290					295					300	
Asn	Ser	Trp	Lys	Ser	Leu	Thr	Ser	Ile	Thr	Leu	Ala	Gly	Asn	Leu	
				305					310					315	
Trp	Asp	Cys	Gly	Arg	Asn	Val	Cys	Ala	Leu	Ala	Ser	Trp	Leu	Ser	
				320					325					330	
Asn	Phe	Gln	Gly	Arg	Tyr	Asp	Gly	Asn	Leu	Gln	Cys	Ala	Ser	Pro	
				335					340					345	
Glu	Tyr	Ala	Gln	Gly	Glu	Asp	Val	Leu	Asp	Ala	Val	Tyr	Ala	Phe	
				350					355					360	
His	Leu	Cys	Glu	Asp	Gly	Ala	Glu	Pro	Thr	Ser	Gly	His	Leu	Leu	
				365					370					375	
Ser	Ala	Val	Thr	Asn	Arg	Ser	Asp	Leu	Gly	Pro	Pro	Ala	Ser	Ser	
				380					385					390	
Ala	Thr	Thr	Leu	Ala	Asp	Gly	Gly	Glu	Gly	Gln	His	Asp	Gly	Thr	
				395					400					405	
Phe	Glu	Pro	Ala	Thr	Val	Ala	Leu	Pro	Gly	Gly	Glu	His	Ala	Glu	
				410					415					420	
Asn	Ala	Val	Gln	Ile	His	Lys	Val	Val	Thr	Gly	Thr	Met	Ala	Leu	
				425					430					435	
Ile	Phe	Ser	Phe	Leu	Ile	Val	Val	Leu	Val	Leu	Tyr	Val	Ser	Trp	
				440					445					450	
Lys	Cys	Phe	Pro	Ala	Ser	Leu	Arg	Gln	Leu	Arg	Gln	Cys	Phe	Val	
				455					460					465	
Thr	Gln	Arg	Arg	Lys	Gln	Lys	Gln	Lys	Gln	Thr	Met	His	Gln	Met	
				470					475					480	
Ala	Ala	Met	Ser	Ala	Gln	Glu	Tyr	Tyr	Val	Asp	Tyr	Lys	Pro	Asn	
				485					490					495	
His	Ile	Glu	Gly	Ala	Leu	Val	Ile	Ile	Asn	Glu	Tyr	Gly	Ser	Cys	
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Thr	Cys	His	Gln	Gln	Pro	Ala	Arg	Glu	Cys	Glu	Val				
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<210> 279

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 279

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<210> 280

<211> 709

<212> DNA

<213> Homo sapiens

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 cacggacttc gacgtcgag ccaactggag ccagaaccgg acccgtgcg 150  
 ccggcggcgc cgttgagttc ccggcggaca agatggtgtc agtcctggtg 200  
 caagaaggtc acgccgtctc agacatgctc ctgccgtgg atggggaact 250  
 cgtcctggct tcaggagccg gattcggcgt ctcagacgtg ggctcgacc 300  
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 cttcttcgtg gacgccgagc gcgtgccctg ccgccacgac gacgtcttct 450  
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 ccagcccct 709

<210> 281  
 <211> 229  
 <212> PRT  
 <213> Homo sapiens

<400> 281  
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 Leu Thr Gln Ala Val Ser Lys Leu Trp Val Pro Asn Thr Asp Phe  
 20 25 30  
 Asp Val Ala Ala Asn Trp Ser Gln Asn Arg Thr Pro Cys Ala Gly  
 35 40 45  
 Gly Ala Val Glu Phe Pro Ala Asp Lys Met Val Ser Val Leu Val  
 50 55 60  
 Gln Glu Gly His Ala Val Ser Asp Met Leu Leu Pro Leu Asp Gly  
 65 70 75  
 Glu Leu Val Leu Ala Ser Gly Ala Gly Phe Gly Val Ser Asp Val  
 80 85 90  
 Gly Ser His Leu Asp Cys Gly Ala Gly Glu Pro Ala Val Phe Arg  
 95 100 105  
 Asp Ser Asp Arg Phe Ser Trp His Asp Pro His Leu Trp Arg Ser  
 110 115 120  
 Gly Asp Glu Ala Pro Gly Leu Phe Phe Val Asp Ala Glu Arg Val  
 125 130 135

Pro Cys Arg His Asp Asp Val Phe Phe Pro Pro Ser Ala Ser Phe  
140 145 150

Arg Val Gly Leu Gly Pro Gly Ala Ser Pro Val Arg Val Arg Ser  
155 160 165

Ile Ser Ala Leu Gly Arg Thr Phe Thr Arg Asp Glu Asp Leu Ala  
170 175 180

Val Phe Leu Ala Ser Arg Ala Gly Arg Leu Arg Phe His Gly Pro  
185 190 195

Gly Ala Leu Ser Val Gly Pro Glu Asp Cys Ala Asp Pro Ser Gly  
200 205 210

Cys Val Cys Gly Asn Ala Glu Ala Gln Pro Trp Ile Cys Ala Ala  
215 220 225

Leu Leu Gln Pro

<210> 282  
<211> 644  
<212> DNA  
<213> Homo sapiens

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tgtgttttgc acttaccctg tgtttctgct tttggtggca taacaaggga 150  
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aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 644

<210> 283  
<211> 77  
<212> PRT  
<213> Homo sapiens

<400> 283  
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Leu Ile Ala Thr Ile Met Val Leu Leu Cys Phe Ala Leu Thr Leu

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Cys Ser Ala Phe	Trp Trp His Asn Lys Gly Leu Ala Leu Ile Phe				
	35		40		45
Cys Ile Leu Gln Ser Leu Ala Leu Thr Trp Tyr Ser Leu Ser Phe					
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Ile Pro Phe Ala Arg Asp Ala Val Lys Lys Cys Phe Ala Val Cys					
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Leu Ala					

<210> 284  
 <211> 2623  
 <212> DNA  
 <213> Homo sapiens

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ggataaaaaa aaaaaaaaaa aaa 2623

<210> 285

**THE**

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**1900**

Met Thr Ser Lys Phe Ile Leu Val Ser Phe Ile Leu Ala Ala Leu  
1 5 10 15

Leu Leu Val Ser Phe Asp Gly Phe Arg Trp Asp Tyr Leu Tyr Lys  
35 40 45

Val Lys Gln Val Thr Asn Val Phe Ile Thr Lys Thr Tyr Pro Asn  
65 70 75

Val Ala Asn Asp Met Phe Asp Pro Ile Arg Asn Lys Ser Phe Ser  
95 100 105

Thr Pro Ile Trp Ile Thr Asn Gln Arg Ala Gly His Thr Ser Gly  
125 130 135

Pro Thr His Tyr Met Pro Tyr Asn Glu Ser Val Ser Phe Glu Asp  
155 160 165

Asn Leu Gly Leu Leu Tyr Trp Glu Asp Pro Asp Asp Met Gly His  
185 190 195

Ile Asp Lys Lys Leu Gly Tyr Leu Ile Gln Met Leu Lys Lys Ala  
215 220 225

Met Thr Gln Cys Ser Glu Glu Arg Leu Ile Glu Leu Asp Gln Tyr  
245 250 255

Ala Ile Leu Pro Lys Glu Gly Lys Phe Asp Glu Val Tyr Glu Ala  
275 280 285

Leu Thr His Ala His Pro Asn Leu Thr Val Tyr Lys Lys Glu Asp



290	295	300
Val Pro Glu Arg Trp His Tyr Lys Tyr	Asn Ser Arg Ile Gln Pro	
305	310	315
Ile Ile Ala Val Ala Asp Glu Gly Trp	His Ile Leu Gln Asn Lys	
320	325	330
Ser Asp Asp Phe Leu Leu Gly Asn His	Gly Tyr Asp Asn Ala Leu	
335	340	345
Ala Asp Met His Pro Ile Phe Leu Ala	His Gly Pro Ala Phe Arg	
350	355	360
Lys Asn Phe Ser Lys Glu Ala Met Asn	Ser Thr Asp Leu Tyr Pro	
365	370	375
Leu Leu Cys His Leu Leu Asn Ile Thr	Ala Met Pro His Asn Gly	
380	385	390
Ser Phe Trp Asn Val Gln Asp Leu Leu	Asn Ser Ala Met Pro Arg	
395	400	405
Val Val Pro Tyr Thr Gln Ser Thr Ile	Leu Leu Pro Gly Ser Val	
410	415	420
Lys Pro Ala Glu Tyr Asp Gln Glu Gly	Ser Tyr Pro Tyr Phe Ile	
425	430	435
Gly Val Ser Leu Gly Ser Ile Ile Val	Ile Val Phe Phe Val Ile	
440	445	450
Phe Ile Lys His Leu Ile His Ser Gln	Ile Pro Ala Leu Gln Asp	
455	460	465
Met His Ala Glu Ile Ala Gln Pro Leu	Leu Gln Ala	
470	475	

<210> 286  
 <211> 1337  
 <212> DNA  
 <213> Homo sapiens

<400> 286  
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 agggaggtga agaaaccaag acgcagagag gccaaagcccc ttgccttggg 150  
 tcacacagcc aaaggaggca gagccagaac tcacaaccag atccagaggc 200  
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 gaagaggagg aggaggagga ggagcagcca ccaccacac cagtctcagg 400  
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 taaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaa 1337

<210> 287  
 <211> 255  
 <212> PRT  
 <213> Homo sapiens

<400> 287  
 Met Ala Thr Trp Asp Glu Lys Ala Val Thr Arg Arg Ala Lys Val  
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 20 25 30  
 Val Gly Asp Asp Tyr His Ala Trp Asn Ile Asn Tyr Lys Lys Trp  
 35 40 45  
 Glu Asn Glu Glu Glu Glu Glu Glu Glu Gln Pro Pro Pro Thr  
 50 55 60  
 Pro Val Ser Gly Glu Glu Gly Arg Ala Ala Ala Pro Asp Val Ala  
 65 70 75  
 Pro Ala Pro Gly Pro Ala Pro Arg Ala Pro Leu Asp Phe Arg Gly  
 80 85 90  
 Met Leu Arg Lys Leu Phe Ser Ser His Arg Phe Gln Val Ile Ile  
 95 100 105  
 Ile Cys Leu Val Val Leu Asp Ala Leu Leu Val Leu Ala Glu Leu  
 110 115 120

Ile	Leu	Asp	Leu	Lys	Ile	Ile	Gln	Pro	Asp	Lys	Asn	Asn	Tyr	Ala
				125					130					135
Ala	Met	Val	Phe	His	Tyr	Met	Ser	Ile	Thr	Ile	Leu	Val	Phe	Phe
				140					145					150
Met	Met	Glu	Ile	Ile	Phe	Lys	Leu	Phe	Val	Phe	Arg	Leu	Ser	Ser
				155					160					165
Phe	Thr	Thr	Ser	Leu	Arg	Ser	Trp	Met	Pro	Val	Val	Val	Val	Val
				170					175					180
Ser	Phe	Ile	Leu	Asp	Ile	Val	Leu	Leu	Phe	Gln	Glu	His	Gln	Phe
				185					190					195
Glu	Ala	Leu	Gly	Leu	Leu	Ile	Leu	Leu	Arg	Leu	Trp	Arg	Val	Ala
				200					205					210
Arg	Ile	Ile	Asn	Gly	Ile	Ile	Ile	Ser	Val	Lys	Thr	Arg	Ser	Glu
				215					220					225
Arg	Gln	Leu	Leu	Arg	Leu	Lys	Gln	Met	Asn	Val	Gln	Leu	Ala	Ala
				230					235					240
Lys	Ile	Gln	His	Leu	Glu	Phe	Ser	Cys	Ser	Glu	Lys	Pro	Leu	Asp
				245					250					255

<210> 288  
 <211> 3334  
 <212> DNA  
 <213> Homo sapiens

<400> 288  
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 cccagaccga gttccagtac tttgagtcga aggggctccc tgccgagctg 150  
 aagtccattt tcaagctcag tgtcttcac ccctcccagg aattctccac 200  
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 aagaagctga ggctggtgtt taagattttg gacaaaaaga atgatggacg 350  
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 acgatgacca tcgactggaa cgagtggaga gactaccacc tcctccaccc 500  
 cgtggaaaac atccccgaga tcctcctcta ctggaagcat tccacgatct 550  
 ttgatgtggg tgagaatcta acgggtcccg atgagttcac agtggaggag 600  
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 ggccgtatcc agaacctgca cggccccctt ggacaggctc aaggtgctca 700  
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gccagtactc aggaatgctg gactgcgcca ggaggatcct ggccagagag 1050  
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 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 3334

<210> 289  
 <211> 469  
 <212> PRT  
 <213> Homo sapiens

<400> 289  
 Met Leu Cys Leu Cys Leu Tyr Val Pro Val Ile Gly Glu Ala Gln  
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 Thr Glu Phe Gln Tyr Phe Glu Ser Lys Gly Leu Pro Ala Glu Leu  
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 Lys Ser Ile Phe Lys Leu Ser Val Phe Ile Pro Ser Gln Glu Phe  
 35 40 45  
 Ser Thr Tyr Arg Gln Trp Lys Gln Lys Ile Val Gln Ala Gly Asp  
 50 55 60  
 Lys Asp Leu Asp Gly Gln Leu Asp Phe Glu Glu Phe Val His Tyr  
 65 70 75  
 Leu Gln Asp His Glu Lys Lys Leu Arg Leu Val Phe Lys Ile Leu  
 80 85 90

Asp	Lys	Lys	Asn	Asp	Gly	Arg	Ile	Asp	Ala	Gln	Glu	Ile	Met	Gln	
			95						100					105	
Ser	Leu	Arg	Asp	Leu	Gly	Val	Lys	Ile	Ser	Glu	Gln	Gln	Ala	Glu	
			110						115					120	
Lys	Ile	Leu	Lys	Ser	Met	Asp	Lys	Asn	Gly	Thr	Met	Thr	Ile	Asp	
			125						130					135	
Trp	Asn	Glu	Trp	Arg	Asp	Tyr	His	Leu	Leu	His	Pro	Val	Glu	Asn	
			140						145					150	
Ile	Pro	Glu	Ile	Ile	Leu	Tyr	Trp	Lys	His	Ser	Thr	Ile	Phe	Asp	
			155						160					165	
Val	Gly	Glu	Asn	Leu	Thr	Val	Pro	Asp	Glu	Phe	Thr	Val	Glu	Glu	
			170						175					180	
Arg	Gln	Thr	Gly	Met	Trp	Trp	Arg	His	Leu	Val	Ala	Gly	Gly	Gly	
			185						190					195	
Ala	Gly	Ala	Val	Ser	Arg	Thr	Cys	Thr	Ala	Pro	Leu	Asp	Arg	Leu	
			200						205					210	
Lys	Val	Leu	Met	Gln	Val	His	Ala	Ser	Arg	Ser	Asn	Asn	Met	Gly	
			215						220					225	
Ile	Val	Gly	Gly	Phe	Thr	Gln	Met	Ile	Arg	Glu	Gly	Gly	Ala	Arg	
			230						235					240	
Ser	Leu	Trp	Arg	Gly	Asn	Gly	Ile	Asn	Val	Leu	Lys	Ile	Ala	Pro	
			245						250					255	
Glu	Ser	Ala	Ile	Lys	Phe	Met	Ala	Tyr	Glu	Gln	Ile	Lys	Arg	Leu	
			260						265					270	
Val	Gly	Ser	Asp	Gln	Glu	Thr	Leu	Arg	Ile	His	Glu	Arg	Leu	Val	
			275						280					285	
Ala	Gly	Ser	Leu	Ala	Gly	Ala	Ile	Ala	Gln	Ser	Ser	Ile	Tyr	Pro	
			290						295					300	
Met	Glu	Val	Leu	Lys	Thr	Arg	Met	Ala	Leu	Arg	Lys	Thr	Gly	Gln	
			305						310					315	
Tyr	Ser	Gly	Met	Leu	Asp	Cys	Ala	Arg	Arg	Ile	Leu	Ala	Arg	Glu	
			320						325					330	
Gly	Val	Ala	Ala	Phe	Tyr	Lys	Gly	Tyr	Val	Pro	Asn	Met	Leu	Gly	
			335						340					345	
Ile	Ile	Pro	Tyr	Ala	Gly	Ile	Asp	Leu	Ala	Val	Tyr	Glu	Thr	Leu	
			350						355					360	
Lys	Asn	Ala	Trp	Leu	Gln	His	Tyr	Ala	Val	Asn	Ser	Ala	Asp	Pro	
			365						370					375	
Gly	Val	Phe	Val	Leu	Leu	Ala	Cys	Gly	Thr	Met	Ser	Ser	Thr	Cys	
			380						385					390	
Gly	Gln	Leu	Ala	Ser	Tyr	Pro	Leu	Ala	Leu	Val	Arg	Thr	Arg	Met	
			395						400					405	

Gln Ala Gln Ala Ser Ile Glu Gly Ala Pro Glu Val Thr Met Ser  
410 415 420

Ser Leu Phe Lys His Ile Leu Arg Thr Glu Gly Ala Phe Gly Leu  
425 430 435

Tyr Arg Gly Leu Ala Pro Asn Phe Met Lys Val Ile Pro Ala Val  
440 445 450

Ser Ile Ser Tyr Val Val Tyr Glu Asn Leu Lys Ile Thr Leu Gly  
455 460 465

Val Gln Ser Arg

<210> 290  
<211> 1658  
<212> DNA  
<213> Homo sapiens

<400> 290  
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atttcaggga gacactccat cacagtcact actgtcgcct cagctgggaa 200  
cattgggggag gatggaatcc tgagctgcac ttttgaacct gacatcaaac 250  
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catgagttca aagaaggcaa agatgagctg tcggagcagg atgaaatgtt 350  
cagaggccgg acagcagtgt ttgctgatca agtgatagtt ggcaatgcct 400  
ctttgcggct gaaaaacgtg caactcacag atgctggcac ctacaaatgt 450  
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tggagccttc agcatgccgg aagtgaatgt ggactataat gccagctcag 550  
agaccttgcg gtgtgaggct ccccgatggt tccccagcc cacagtggtc 600  
tgggcatccc aagttgacca gggagccaac ttctcggaag tctccaatac 650  
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tctacaatgt tacgatcaac aacacatact cctgtatgat tgaaaatgac 750  
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gcggagtcac ctacagctgc taaactcaaa ggcttctctg tgtgtctctt 850  
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acagggatct acagaactat ttcaccacca gatatgacct agttttatat 1000  
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 tgtaatgttg ctctgaggaa gcccttgaa agtctatccc aacatatcca 1350  
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 aattgactgc cacttcgcaa ctcaggggag gctgcatttt agtaatgggt 1450  
 caaatgattc actttttatg atgcttccaa aggtgccttg gcttctcttc 1500  
 ccaactgaca aatgccaaag ttgagaaaaa tgatcataat tttagcataa 1550  
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 aaaaaaaaa 1658

<210> 291  
 <211> 282  
 <212> PRT  
 <213> Homo sapiens

<400> 291  
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 20 25 30  
 Ile Ser Gly Arg His Ser Ile Thr Val Thr Thr Val Ala Ser Ala  
 35 40 45  
 Gly Asn Ile Gly Glu Asp Gly Ile Leu Ser Cys Thr Phe Glu Pro  
 50 55 60  
 Asp Ile Lys Leu Ser Asp Ile Val Ile Gln Trp Leu Lys Glu Gly  
 65 70 75  
 Val Leu Gly Leu Val His Glu Phe Lys Glu Gly Lys Asp Glu Leu  
 80 85 90  
 Ser Glu Gln Asp Glu Met Phe Arg Gly Arg Thr Ala Val Phe Ala  
 95 100 105  
 Asp Gln Val Ile Val Gly Asn Ala Ser Leu Arg Leu Lys Asn Val  
 110 115 120  
 Gln Leu Thr Asp Ala Gly Thr Tyr Lys Cys Tyr Ile Ile Thr Ser  
 125 130 135  
 Lys Gly Lys Gly Asn Ala Asn Leu Glu Tyr Lys Thr Gly Ala Phe  
 140 145 150  
 Ser Met Pro Glu Val Asn Val Asp Tyr Asn Ala Ser Ser Glu Thr



	155		160		165
Leu Arg Cys Glu	Ala Pro Arg Trp Phe	Pro Gln Pro Thr Val	Val		
	170	175	180		
Trp Ala Ser Gln	Val Asp Gln Gly Ala	Asn Phe Ser Glu Val	Ser		
	185	190	195		
Asn Thr Ser Phe	Glu Leu Asn Ser Glu	Asn Val Thr Met Lys	Val		
	200	205	210		
Val Ser Val Leu	Tyr Asn Val Thr Ile	Asn Asn Thr Tyr Ser	Cys		
	215	220	225		
Met Ile Glu Asn	Asp Ile Ala Lys Ala	Thr Gly Asp Ile Lys	Val		
	230	235	240		
Thr Glu Ser Glu	Ile Lys Arg Arg Ser	His Leu Gln Leu Leu	Asn		
	245	250	255		
Ser Lys Ala Ser	Leu Cys Val Ser Ser	Phe Phe Ala Ile Ser	Trp		
	260	265	270		
Ala Leu Leu Pro	Leu Ser Pro Tyr Leu	Met Leu Lys			
	275	280			

<210> 292  
 <211> 1484  
 <212> DNA  
 <213> Homo sapiens

<400> 292  
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 cagcagttgc tacaggagat gaagaccctc ttcttgaata ctgagtacct 200  
 gatgcccttt ctctcaacc agtgtggatc ccttctctat tacctcacct 250  
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 aaaacgtaag ttagactact gcgagtgcgg gacgcagctc tgttgatctc 400  
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 aatttcaact tgcatacaca gctcagtgag taagaccag gggcaacagt 750  
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gccctgaggc catgaagtgc tggcagtgag cggatggacc tagcacttcc 850  
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 aacctttctg cccagcagc tctcttctg ctaacatctc aggctcccag 1050  
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 agccagaaat gcaaacggga ggcctctggg actcagtcag agcgctttgg 1200  
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 cagccccacc tgactccagc acacctggcg agtagtagct gtcaataaat 1400  
 ctatgtaaac agacaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1450  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaa 1484

<210> 293  
 <211> 180  
 <212> PRT  
 <213> Homo sapiens

<400> 293  
 Met Ala Ala Ser Leu Gly Gln Val Leu Ala Leu Val Leu Val Ala  
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 Ala Leu Trp Gly Gly Thr Gln Pro Leu Leu Lys Arg Ala Ser Ala  
 20 25 30  
 Gly Leu Gln Arg Val His Glu Pro Thr Trp Ala Gln Gln Leu Leu  
 35 40 45  
 Gln Glu Met Lys Thr Leu Phe Leu Asn Thr Glu Tyr Leu Met Pro  
 50 55 60  
 Phe Leu Leu Asn Gln Cys Gly Ser Leu Leu Tyr Tyr Leu Thr Leu  
 65 70 75  
 Ala Ser Thr Asp Leu Thr Leu Ala Val Pro Ile Cys Asn Ser Leu  
 80 85 90  
 Ala Ile Ile Phe Thr Leu Ile Val Gly Lys Ala Leu Gly Glu Asp  
 95 100 105  
 Ile Gly Gly Lys Arg Lys Leu Asp Tyr Cys Glu Cys Gly Thr Gln  
 110 115 120  
 Leu Cys Gly Ser Arg His Thr Cys Val Ser Ser Phe Pro Glu Pro  
 125 130 135  
 Ile Ser Pro Glu Trp Val Arg Thr Arg Pro Phe Pro Ile Leu Pro  
 140 145 150

Phe	Pro	Leu	Gln	Leu	Phe	Cys	Phe	Leu	Val	Ala	Ile	Arg	Val	Pro
				155					160					165
Phe	Pro	Trp	Thr	Val	Trp	Arg	Lys	Thr	Glu	Ala	Gly	Val	Trp	Asp
				170					175					180

<210> 294  
 <211> 1164  
 <212> DNA  
 <213> Homo sapiens

<400> 294  
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 gctttctctg tggaagatga cagcaattat agcaggaccc tgccaggctg 100  
 tcgaaaagat tccgcaataa aactttgcca gtgggaagta cctagtgaaa 150  
 cggcctaaga tgccacttct tctcatgtcc caggcttgag gccctgtggt 200  
 ccccatcctt gggagaagtc agctccagca ccatgaaggg catcctcggt 250  
 gctggtatca ctgcagtgct tgttgcagct gtagaatctc tgagctgcgt 300  
 gcagtgtaat tcatgggaaa aatcctgtgt caacagcatt gcctctgaat 350  
 gtccctcaca tgccaacacc agctgtatca gtcctcagc cagctcctct 400  
 ctagagacac cagtcagatt ataccagaat atgttctgct cagcggagaa 450  
 ctgcagtgag gagacacaca ttacagcctt cactgtccac gtgtctgctg 500  
 aagaacactt tcattttgta agccagtgtg gccaaaggaaa ggaatgcagc 550  
 aacaccagcg atgccctgga ccttcccctg aagaacgtgt ccagcaacgc 600  
 agagtgccct gcttggtatg aatctaattg aacttcctgt cgtgggaagc 650  
 cctggaaatg ctatgaagaa gaacagtgtg tctttctagt tgcagaactt 700  
 aagaatgaca ttgagtctaa gagtctcgtg ctgaaaggct gttccaacgt 750  
 cagtaacgcc acctgtcagt tctgtctggt tgaaaacaag actcttgag 800  
 gagtcattct tcgaaagttt gagtgtgcaa atgtaaacag cttaccccc 850  
 acgtctgcac caaccacttc ccacaacgtg ggctccaaag cttccctcta 900  
 cctcttggcc cttgccagcc tcttctctcg gggactgctg cctgaggtc 950  
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 ctgcccagta agtgggagtc acaggtctcc aggcaatgcc gacagctgcc 1100  
 ttgttcttca ttattaaagc actggttcat tcaactgcaa aaaaaaaaaa 1150  
 aaaaaaaaaa aaaa 1164

<210> 295  
 <211> 237  
 <212> PRT

<213> Homo sapiens

<400> 295

Met Lys Gly Ile Leu Val Ala Gly Ile Thr Ala Val Leu Val Ala  
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Ala Val Glu Ser Leu Ser Cys Val Gln Cys Asn Ser Trp Glu Lys  
20 25 30  
Ser Cys Val Asn Ser Ile Ala Ser Glu Cys Pro Ser His Ala Asn  
35 40 45  
Thr Ser Cys Ile Ser Ser Ser Ala Ser Ser Ser Leu Glu Thr Pro  
50 55 60  
Val Arg Leu Tyr Gln Asn Met Phe Cys Ser Ala Glu Asn Cys Ser  
65 70 75  
Glu Glu Thr His Ile Thr Ala Phe Thr Val His Val Ser Ala Glu  
80 85 90  
Glu His Phe His Phe Val Ser Gln Cys Cys Gln Gly Lys Glu Cys  
95 100 105  
Ser Asn Thr Ser Asp Ala Leu Asp Pro Pro Leu Lys Asn Val Ser  
110 115 120  
Ser Asn Ala Glu Cys Pro Ala Cys Tyr Glu Ser Asn Gly Thr Ser  
125 130 135  
Cys Arg Gly Lys Pro Trp Lys Cys Tyr Glu Glu Glu Gln Cys Val  
140 145 150  
Phe Leu Val Ala Glu Leu Lys Asn Asp Ile Glu Ser Lys Ser Leu  
155 160 165  
Val Leu Lys Gly Cys Ser Asn Val Ser Asn Ala Thr Cys Gln Phe  
170 175 180  
Leu Ser Gly Glu Asn Lys Thr Leu Gly Gly Val Ile Phe Arg Lys  
185 190 195  
Phe Glu Cys Ala Asn Val Asn Ser Leu Thr Pro Thr Ser Ala Pro  
200 205 210  
Thr Thr Ser His Asn Val Gly Ser Lys Ala Ser Leu Tyr Leu Leu  
215 220 225  
Ala Leu Ala Ser Leu Leu Leu Arg Gly Leu Leu Pro  
230 235

<210> 296

<211> 1245

<212> DNA

<213> Homo sapiens

<400> 296

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aatctggggtc	cccgggcggc	ggggggcccaa	ggcctgaccc	agactccgac	200
cgaaatgcag	cgggtcagtt	tacgcttttg	gggccccatg	accgcgagct	250
accggagcac	cgcccggact	ggtcttcccc	ggaagacaag	gataatccta	300
gaggacgaga	atgatgccat	ggccgacgcc	gaccgcctgg	ctggaccagc	350
ggctgccgag	ctcttgccg	ccacgggtgtc	caccgggcttt	agccgggtcgt	400
ccgccattaa	cgaggaggat	gggtcttcag	aagaggggggt	tgtgattaat	450
gccggaaaag	atagcaccag	cagagagctt	cccagtgcga	ctcccaatac	500
agcggggagt	tccagcacga	ggtttatagc	caatagtcag	gagcctgaaa	550
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ctgccagggt	cgcaggccac	cctgagccag	tggtccacac	ctgggtctac	650
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gcgccttcga	gttggggcgc	tgagccagct	ccgcacggag	cacaagcctt	850
gcacctatca	acaatgtccc	tgcaaccgac	ttcggaaga	gtgccccctg	900
gacacaagtc	tctgtactga	caccaactgt	gcctctcaga	gcaccaccag	950
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ccagcctgcc	acccgccagc	ccctgcccag	ccctgggcttt	ttggaaacgg	1050
gtcaggattg	gcctggagga	tatttggaat	agcctctctt	cagtgttcac	1100
agagatgcaa	ccaatagaca	gaaaccagag	gtaatggcca	cttcatccac	1150
atgaggagat	gtcagtatct	caacctctct	tgccctttca	atcctagcac	1200
ccactagata	tttttagtac	agaaaaacaa	aactggaaaa	cacaa	1245

<210> 297

<212> PRT

<400> 297

Leu Gly Pro Arg Ala Ala Gly Ala Gln Gly Leu Thr Gln Thr Pro  
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Arg Ser Tyr Arg Ser Thr Ala Arg Thr Gly Leu Pro Arg Lys Thr  
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	65		70		75
Arg Leu Ala Gly	Pro 80	Ala Ala Ala Glu	Leu 85	Leu Ala Ala Thr	Val 90
Ser Thr Gly Phe	Ser 95	Arg Ser Ser Ala	Ile 100	Asn Glu Glu Asp	Gly 105
Ser Ser Glu Glu	Gly 110	Val Val Ile Asn	Ala 115	Gly Lys Asp Ser	Thr 120
Ser Arg Glu Leu	Pro 125	Ser Ala Thr Pro	Asn 130	Thr Ala Gly Ser	Ser 135
Ser Thr Arg Phe	Ile 140	Ala Asn Ser Gln	Glu 145	Pro Glu Ile Arg	Leu 150
Thr Ser Ser Leu	Pro 155	Arg Ser Pro Gly	Arg 160	Ser Thr Glu Asp	Leu 165
Pro Gly Ser Gln	Ala 170	Thr Leu Ser Gln	Trp 175	Ser Thr Pro Gly	Ser 180
Thr Pro Ser Arg	Trp 185	Pro Ser Pro Ser	Pro 190	Thr Ala Met Pro	Ser 195
Pro Glu Asp Leu	Arg 200	Leu Val Leu Met	Pro 205	Trp Gly Pro Trp	His 210
Cys His Cys Lys	Ser 215	Gly Thr Met Ser	Arg 220	Ser Arg Ser Gly	Lys 225
Leu His Gly Leu	Ser 230	Gly Arg Leu Arg	Val 235	Gly Ala Leu Ser	Gln 240
Leu Arg Thr Glu	His 245	Lys Pro Cys Thr	Tyr 250	Gln Gln Cys Pro	Cys 255
Asn Arg Leu Arg	Glu 260	Glu Cys Pro Leu	Asp 265	Thr Ser Leu Cys	Thr 270
Asp Thr Asn Cys	Ala 275	Ser Gln Ser Thr	Thr 280	Ser Thr Arg Thr	Thr 285
Thr Thr Pro Phe	Pro 290	Thr Ile His Leu	Arg 295	Ser Ser Pro Ser	Leu 300
Pro Pro Ala Ser	Pro 305	Cys Pro Ala Leu	Ala 310	Phe Trp Lys Arg	Val 315
Arg Ile Gly Leu	Glu 320	Asp Ile Trp Asn	Ser 325	Leu Ser Ser Val	Phe 330
Thr Glu Met Gln	Pro 335	Ile Asp Arg Asn	Gln 340	Arg	

<210> 298  
<211> 2692  
<212> DNA  
<213> Homo sapiens

<400> 298  
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[illegible]

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gtgcgcagtg	tggagacggg	tgttgtcggg	gaagaggtgt	ggcttcaaag	1800
tgtgtgtgtg	caggggggtg	gtgtgttagc	gtgggttagg	ggaacgtgtg	1850
tgcgcgtgct	ggtgggcatg	tgagatgagt	gactgccggt	gaatgtgtcc	1900
acagttgaga	ggttgagca	ggatgagggg	atcctgtcac	catcaataat	1950
cacttgtgga	gcgccagctc	tgcccaagac	gccacctggg	cggacagcca	2000
ggagctctcc	atggccaggc	tgcctgtgtg	catgttccct	gtctggtgcc	2050
cctttgcccg	cctcctgcaa	acctcacagg	gtccccacac	aacagtgcc	2100
tccagaagca	gccccctgga	ggcagaggaa	ggaaaatggg	gatggctggg	2150
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tccaaaacct	ccattccct	gctgccagcc	cctttgccat	agcctgattt	2250
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gcagactgga	tttttgctct	gcccctgacc	ccttgctcct	ctttgagggg	2550
ggggagctat	gctaggactc	caacctcagg	gactcgggtg	gocctgcgcta	2600
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<210> 299

<211> 320

&lt;212&gt; PRT

<213> Homo sapiens

<400> 299

Met Ala Gly Leu Ala Ala Arg Leu Val Leu Leu Ala Gly Ala Ala  
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Asp Cys Val Leu Gln Cys Glu Glu Gln Asn Cys Ser Gly Gly Ala  
35 40 45

Leu Asn His Phe Arg Ser Arg Gln Pro Ile Tyr Met Ser Leu Ala  
50 55 60

Gly Trp Thr Cys Arg Asp Asp Cys Lys Tyr Glu Cys Met Trp Val  
65 70 75



Thr	Val	Gly	Leu	Tyr	Leu	Gln	Glu	Gly	His	Lys	Val	Pro	Gln	Phe	
				80					85					90	
His	Gly	Lys	Trp	Pro	Phe	Ser	Arg	Phe	Leu	Phe	Phe	Gln	Glu	Pro	
				95					100					105	
Ala	Ser	Ala	Val	Ala	Ser	Phe	Leu	Asn	Gly	Leu	Ala	Ser	Leu	Val	
				110					115					120	
Met	Leu	Cys	Arg	Tyr	Arg	Thr	Phe	Val	Pro	Ala	Ser	Ser	Pro	Met	
				125					130					135	
Tyr	His	Thr	Cys	Val	Ala	Phe	Ala	Trp	Val	Ser	Leu	Asn	Ala	Trp	
				140					145					150	
Phe	Trp	Ser	Thr	Val	Phe	His	Thr	Arg	Asp	Thr	Asp	Leu	Thr	Glu	
				155					160					165	
Lys	Met	Asp	Tyr	Phe	Cys	Ala	Ser	Thr	Val	Ile	Leu	His	Ser	Ile	
				170					175					180	
Tyr	Leu	Cys	Cys	Val	Arg	Thr	Val	Gly	Leu	Gln	His	Pro	Ala	Val	
				185					190					195	
Val	Ser	Ala	Phe	Arg	Ala	Leu	Leu	Leu	Leu	Met	Leu	Thr	Val	His	
				200					205					210	
Val	Ser	Tyr	Leu	Ser	Leu	Ile	Arg	Phe	Asp	Tyr	Gly	Tyr	Asn	Leu	
				215					220					225	
Val	Ala	Asn	Val	Ala	Ile	Gly	Leu	Val	Asn	Val	Val	Trp	Trp	Leu	
				230					235					240	
Ala	Trp	Cys	Leu	Trp	Asn	Gln	Arg	Arg	Leu	Pro	His	Val	Arg	Lys	
				245					250					255	
Cys	Val	Val	Val	Val	Leu	Leu	Leu	Gln	Gly	Leu	Ser	Leu	Leu	Glu	
				260					265					270	
Leu	Leu	Asp	Phe	Pro	Pro	Leu	Phe	Trp	Val	Leu	Asp	Ala	His	Ala	
				275					280					285	
Ile	Trp	His	Ile	Ser	Thr	Ile	Pro	Val	His	Val	Leu	Phe	Phe	Ser	
				290					295					300	
Phe	Leu	Glu	Asp	Asp	Ser	Leu	Tyr	Leu	Leu	Lys	Glu	Ser	Glu	Asp	
				305					310					315	
Lys	Phe	Lys	Leu	Asp											
				320											

<210> 300  
 <211> 1674  
 <212> DNA  
 <213> Homo sapiens

<400> 300  
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cctcagtcac cagaacctga aggagtttgc cctgaccaac ccagagaaga 200  
 gcagcaccaa agaaacggag agaaaagaaa ccaaagccga ggaggagctg 250  
 gatgccgaag tcctggaggt gttccaccog acgcatgagt ggcaggccct 300  
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 aatttgaaag gcaaaaggct ggatatcaac accaacacct acacatctca 450  
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 gctccagttt ggaagagaag attgctgcgc tctttgatct tgaatattat 700  
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 gaggccatcg aagggggagc cctgcagaag ctgctgggtca tcctggccac 900  
 ggagcagccg ctactgcaa agaagaaggt cctgtttgca ctgtgctccc 950  
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 ctgcaggctc tgaggacct ggtgcaggag aagggcacgg aggtgctcgc 1050  
 cgtgcgcgtg gtcacactgc tctacgacct ggtcacggag aagatgttcg 1100  
 ccgaggagga ggctgagctg acccaggaga tgtcccaga gaagctgcag 1150  
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 ccagggtctg gccagcctgg agctgcagga tggtagaggac gagggctact 1400  
 tccaggagct gctgggctct gtcaacagct tgetgaagga gctgagatga 1450  
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 ccagcgtggg tgggcttctc aggcaggagg acatcttggc agtgctggct 1550  
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 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1650  
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<210> 301

<211> 461  
 <212> PRT  
 <213> Homo sapiens

<400> 301

Met	Ala	Pro	Gln	Ser	Leu	Pro	Ser	Ser	Arg	Met	Ala	Pro	Leu	Gly	1	5	10	15
Met	Leu	Leu	Gly	Leu	Leu	Met	Ala	Ala	Cys	Phe	Thr	Phe	Cys	Leu	20	25	30	
Ser	His	Gln	Asn	Leu	Lys	Glu	Phe	Ala	Leu	Thr	Asn	Pro	Glu	Lys	35	40	45	
Ser	Ser	Thr	Lys	Glu	Thr	Glu	Arg	Lys	Glu	Thr	Lys	Ala	Glu	Glu	50	55	60	
Glu	Leu	Asp	Ala	Glu	Val	Leu	Glu	Val	Phe	His	Pro	Thr	His	Glu	65	70	75	
Trp	Gln	Ala	Leu	Gln	Pro	Gly	Gln	Ala	Val	Pro	Ala	Gly	Ser	His	80	85	90	
Val	Arg	Leu	Asn	Leu	Gln	Thr	Gly	Glu	Arg	Glu	Ala	Lys	Leu	Gln	95	100	105	
Tyr	Glu	Asp	Lys	Phe	Arg	Asn	Asn	Leu	Lys	Gly	Lys	Arg	Leu	Asp	110	115	120	
Ile	Asn	Thr	Asn	Thr	Tyr	Thr	Ser	Gln	Asp	Leu	Lys	Ser	Ala	Leu	125	130	135	
Ala	Lys	Phe	Lys	Glu	Gly	Ala	Glu	Met	Glu	Ser	Ser	Lys	Glu	Asp	140	145	150	
Lys	Ala	Arg	Gln	Ala	Glu	Val	Lys	Arg	Leu	Phe	Arg	Pro	Ile	Glu	155	160	165	
Glu	Leu	Lys	Lys	Asp	Phe	Asp	Glu	Leu	Asn	Val	Val	Ile	Glu	Thr	170	175	180	
Asp	Met	Gln	Ile	Met	Val	Arg	Leu	Ile	Asn	Lys	Phe	Asn	Ser	Ser	185	190	195	
Ser	Ser	Ser	Leu	Glu	Glu	Lys	Ile	Ala	Ala	Leu	Phe	Asp	Leu	Glu	200	205	210	
Tyr	Tyr	Val	His	Gln	Met	Asp	Asn	Ala	Gln	Asp	Leu	Leu	Ser	Phe	215	220	225	
Gly	Gly	Leu	Gln	Val	Val	Ile	Asn	Gly	Leu	Asn	Ser	Thr	Glu	Pro	230	235	240	
Leu	Val	Lys	Glu	Tyr	Ala	Ala	Phe	Val	Leu	Gly	Ala	Ala	Phe	Ser	245	250	255	
Ser	Asn	Pro	Lys	Val	Gln	Val	Glu	Ala	Ile	Glu	Gly	Gly	Ala	Leu	260	265	270	
Gln	Lys	Leu	Leu	Val	Ile	Leu	Ala	Thr	Glu	Gln	Pro	Leu	Thr	Ala	275	280	285	
Lys	Lys	Lys	Val	Leu	Phe	Ala	Leu	Cys	Ser	Leu	Leu	Arg	His	Phe				

290	295	300
Pro Tyr Ala Gln Arg Gln Phe Leu Lys Leu Gly Gly Leu Gln Val		
305	310	315
Leu Arg Thr Leu Val Gln Glu Lys Gly Thr Glu Val Leu Ala Val		
320	325	330
Arg Val Val Thr Leu Leu Tyr Asp Leu Val Thr Glu Lys Met Phe		
335	340	345
Ala Glu Glu Glu Ala Glu Leu Thr Gln Glu Met Ser Pro Glu Lys		
350	355	360
Leu Gln Gln Tyr Arg Gln Val His Leu Leu Pro Gly Leu Trp Glu		
365	370	375
Gln Gly Trp Cys Glu Ile Thr Ala His Leu Leu Ala Leu Pro Glu		
380	385	390
His Asp Ala Arg Glu Lys Val Leu Gln Thr Leu Gly Val Leu Leu		
395	400	405
Thr Thr Cys Arg Asp Arg Tyr Arg Gln Asp Pro Gln Leu Gly Arg		
410	415	420
Thr Leu Ala Ser Leu Gln Ala Glu Tyr Gln Val Leu Ala Ser Leu		
425	430	435
Glu Leu Gln Asp Gly Glu Asp Glu Gly Tyr Phe Gln Glu Leu Leu		
440	445	450
Gly Ser Val Asn Ser Leu Leu Lys Glu Leu Arg		
455	460	

<210> 302  
 <211> 2136  
 <212> DNA  
 <213> Homo sapiens

<400> 302  
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 tcccatttgc ctgtcctggt caggccccca ccccccttc cacctgacca 200  
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 ggggttagcat cgctgagtga ggacggaaga tcacccatct ccatccgcca 550

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atggtgtatt ctgccctgcg catccacacc gaggactgag ggaacctagg 1350  
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tagccattgc cctggagatg aaattaatgg aggctcaagg atagatgagc 1500  
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ggtggagtgt cccatccttt taatcaaggt gattgtgatt ttgactaata 2050  
aaaaagaatt tgtaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2100  
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 2136

<210> 303  
 <211> 247  
 <212> PRT  
 <213> Homo sapiens

<400> 303

Met	Gly	Ala	Ala	Val	Phe	Phe	Gly	Cys	Thr	Phe	Val	Ala	Phe	Gly	1	5	10	15
Pro	Ala	Phe	Ala	Leu	Phe	Leu	Ile	Thr	Val	Ala	Gly	Asp	Pro	Leu	20	25	30	
Arg	Val	Ile	Ile	Leu	Val	Ala	Gly	Ala	Phe	Phe	Trp	Leu	Val	Ser	35	40	45	
Leu	Leu	Leu	Ala	Ser	Val	Val	Trp	Phe	Ile	Leu	Val	His	Val	Thr	50	55	60	
Asp	Arg	Ser	Asp	Ala	Arg	Leu	Gln	Tyr	Gly	Leu	Leu	Ile	Phe	Gly	65	70	75	
Ala	Ala	Val	Ser	Val	Leu	Leu	Gln	Glu	Val	Phe	Arg	Phe	Ala	Tyr	80	85	90	
Tyr	Lys	Leu	Leu	Lys	Lys	Ala	Asp	Glu	Gly	Leu	Ala	Ser	Leu	Ser	95	100	105	
Glu	Asp	Gly	Arg	Ser	Pro	Ile	Ser	Ile	Arg	Gln	Met	Ala	Tyr	Val	110	115	120	
Ser	Gly	Leu	Ser	Phe	Gly	Ile	Ile	Ser	Gly	Val	Phe	Ser	Val	Ile	125	130	135	
Asn	Ile	Leu	Ala	Asp	Ala	Leu	Gly	Pro	Gly	Val	Val	Gly	Ile	His	140	145	150	
Gly	Asp	Ser	Pro	Tyr	Tyr	Phe	Leu	Thr	Ser	Ala	Phe	Leu	Thr	Ala	155	160	165	
Ala	Ile	Ile	Leu	Leu	His	Thr	Phe	Trp	Gly	Val	Val	Phe	Phe	Asp	170	175	180	
Ala	Cys	Glu	Arg	Arg	Arg	Tyr	Trp	Ala	Leu	Gly	Leu	Val	Val	Gly	185	190	195	
Ser	His	Leu	Leu	Thr	Ser	Gly	Leu	Thr	Phe	Leu	Asn	Pro	Trp	Tyr	200	205	210	
Glu	Ala	Ser	Leu	Leu	Pro	Ile	Tyr	Ala	Val	Thr	Val	Ser	Met	Gly	215	220	225	
Leu	Trp	Ala	Phe	Ile	Thr	Ala	Gly	Gly	Ser	Leu	Arg	Ser	Ile	Gln	230	235	240	
Arg	Ser	Leu	Leu	Cys	Lys	Asp	245											

<210> 304  
 <211> 240  
 <212> DNA  
 <213> Homo sapiens

<220>

<221> unsure  
<222> 108, 123, 126, 154, 198, 206, 217  
<223> unknown base

<400> 304  
aagctggttt aaggaagcag aggaggggta gattcggtga gtgaggacgg 50  
aagatcaacc catttccatt ccgccagatg gcctatgttt ctggtctctc 100  
ccttcggnat catcagtggg gtnttntctg ttatcaatat ttgggctgat 150  
gcanttgggc caggtgtggg tgggatccat ggagactcac cctattantt 200  
cctganttca gccttntga cagcagccat tatcctgctc 240

<210> 305  
<211> 378  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 58, 94, 132, 186, 191, 220, 240, 248, 280, 311, 332  
<223> unknown base

<400> 305  
gaccgaccgt tcagatgccc ggttccagta cggcttcctg atttttggtg 50  
ctgctgtntc tgtccttcta caggaggtgt tccgctttgc ctantacaag 100  
ctgcttaaga aggcagatga ggggttagca tngctgagtg aggacggaag 150  
atcacccatt tccatccgcc agatggccta tgtttntggg ntttccttcg 200  
gtatcatcag tgggtgtttt tctgttatca atattttggn tgatgcantt 250  
gggccagggtg tgggtgggat ccatggagan tcacctatt aattcctgaa 300  
ttcagccttt ntgacagcag ccattatcct gntccatacc ttttggggag 350  
ttgtgttttt tgatgcctgt gagaggag 378

<210> 306  
<211> 655  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 1, 22, 129, 133, 184  
<223> unknown base

<400> 306  
ngttggagaa gtggcgcgga cnttcatttg gggtttcggg tccccccctt 50  
tccctttccc cggggtctgg ggtgacattg cacggggccc tcgtgggggc 100  
gcgttgccac cccacgcgga ctccccagnt ggngcgccct tcccatttgc 150  
ctgtcctggg caggccccca ccccccttcc caentgacca gccatggggg 200  
ctgcggtgtt tttcggctgc actttogtgc cgttcggccc ggccttcgcg 250





aggaggaggc agtggccagg aaggcacagg cctgagaagt ctgcggctga 100  
 gctgggagca aatccccac cccctacctg ggggacagg caagtgagac 150  
 ctggtgaggg tggctcagca ggcagggaag gagaggtgtc tgtgcgtcct 200  
 gcaccacat ctttctctgt cccctccttg ccctgtctgg aggctgctag 250  
 actcctatct tctgaattct atagtgcctg ggtctcagcg cagtgccgat 300  
 ggtggcccg ccttgtggtt cctctctacc tggggaaata aggtgcagcg 350  
 gccatggcta cagcaagacc cccctggatg tgggtgctct gtgctctgat 400  
 cacagccttg cttctggggg tcacagagca tgttctcgcc aacaatgatg 450  
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 cgctgttgct aaggccaac cagctctact gggggcggt gttggtgcat 650  
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 agtggatcca ggaaaccatc caggccaact cctgagtcac cccaggactc 1250  
 agcacaccgg catccccacc tgctgcaggg acagccctga cactcctttc 1300  
 agaccctcat tccttcccag agatgttgag aatgttcac tcctccagccc 1350  
 ctgaccccat gtctcctgga ctccagggtct gcttcccca cattgggctg 1400  
 accgtgtctc tctagttaa ccctgggaac aatttccaaa actgtccagg 1450  
 gcgggggttg cgtctcaatc tccctggggc actttcatcc tcaagctcag 1500  
 ggcccatccc ttctctgcag ctctgaccca aatttagtcc cagaaataaa 1550  
 ctgagaagtg gaaaaaaaaa 1570

<210> 309

<211> 293  
 <212> PRT  
 <213> Homo sapiens

<400> 309

Met	Ala	Thr	Ala	Arg	Pro	Pro	Trp	Met	Trp	Val	Leu	Cys	Ala	Leu	1	5	10	15
Ile	Thr	Ala	Leu	Leu	Leu	Gly	Val	Thr	Glu	His	Val	Leu	Ala	Asn	20	25	30	
Asn	Asp	Val	Ser	Cys	Asp	His	Pro	Ser	Asn	Thr	Val	Pro	Ser	Gly	35	40	45	
Ser	Asn	Gln	Asp	Leu	Gly	Ala	Gly	Ala	Gly	Glu	Asp	Ala	Arg	Ser	50	55	60	
Asp	Asp	Ser	Ser	Ser	Arg	Ile	Ile	Asn	Gly	Ser	Asp	Cys	Asp	Met	65	70	75	
His	Thr	Gln	Pro	Trp	Gln	Ala	Ala	Leu	Leu	Leu	Arg	Pro	Asn	Gln	80	85	90	
Leu	Tyr	Cys	Gly	Ala	Val	Leu	Val	His	Pro	Gln	Trp	Leu	Leu	Thr	95	100	105	
Ala	Ala	His	Cys	Arg	Lys	Lys	Val	Phe	Arg	Val	Arg	Leu	Gly	His	110	115	120	
Tyr	Ser	Leu	Ser	Pro	Val	Tyr	Glu	Ser	Gly	Gln	Gln	Met	Phe	Gln	125	130	135	
Gly	Val	Lys	Ser	Ile	Pro	His	Pro	Gly	Tyr	Ser	His	Pro	Gly	His	140	145	150	
Ser	Asn	Asp	Leu	Met	Leu	Ile	Lys	Leu	Asn	Arg	Arg	Ile	Arg	Pro	155	160	165	
Thr	Lys	Asp	Val	Arg	Pro	Ile	Asn	Val	Ser	Ser	His	Cys	Pro	Ser	170	175	180	
Ala	Gly	Thr	Lys	Cys	Leu	Val	Ser	Gly	Trp	Gly	Thr	Thr	Lys	Ser	185	190	195	
Pro	Gln	Val	His	Phe	Pro	Lys	Val	Leu	Gln	Cys	Leu	Asn	Ile	Ser	200	205	210	
Val	Leu	Ser	Gln	Lys	Arg	Cys	Glu	Asp	Ala	Tyr	Pro	Arg	Gln	Ile	215	220	225	
Asp	Asp	Thr	Met	Phe	Cys	Ala	Gly	Asp	Lys	Ala	Gly	Arg	Asp	Ser	230	235	240	
Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Val	Val	Cys	Asn	Gly	Ser	Leu	245	250	255	
Gln	Gly	Leu	Val	Ser	Trp	Gly	Asp	Tyr	Pro	Cys	Ala	Arg	Pro	Asn	260	265	270	
Arg	Pro	Gly	Val	Tyr	Thr	Asn	Leu	Cys	Lys	Phe	Thr	Lys	Trp	Ile	275	280	285	
Gln	Glu	Thr	Ile	Gln	Ala	Asn	Ser											

<210> 310  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 310  
 tcctgtgacc acccctctaa cacc 24

<210> 311  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 311  
 ctggaacatc tgctgcccag attc 24

<210> 312  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 312  
 gtcggatgac agcagcagcc gcatcatcaa tggatccgac tgcgatatgc 50

<210> 313  
 <211> 3010  
 <212> DNA  
 <213> Homo sapiens

<400> 313  
 atggtcaacg accggtggaa gaccatgggc ggcgctgccc aacttgagga 50  
 ccggccgcgc gacaagccgc agcggccgag ctgcggctac gtgctgtgca 100  
 ccgtgctgct ggccctggct gtgctgctgg ctgtagctgt caccggtgcc 150  
 gtgctcttcc tgaaccacgc ccacgcgccg ggcacggcgc cccacctgt 200  
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gggagaggcc gtgtgacctg gctctctgtc ccagtgccac caggtcatcc 3000  
acatgcgcag 3010

<210> 314  
<211> 461  
<212> PRT  
<213> Homo sapiens

<400> 314  
Met Val Asn Asp Arg Trp Lys Thr Met Gly Gly Ala Ala Gln Leu  
1 5 10 15  
Glu Asp Arg Pro Arg Asp Lys Pro Gln Arg Pro Ser Cys Gly Tyr  
20 25 30  
Val Leu Cys Thr Val Leu Leu Ala Leu Ala Val Leu Leu Ala Val  
35 40 45  
Ala Val Thr Gly Ala Val Leu Phe Leu Asn His Ala His Ala Pro  
50 55 60  
Gly Thr Ala Pro Pro Pro Val Val Ser Thr Gly Ala Ala Ser Ala  
65 70 75  
Asn Ser Ala Leu Val Thr Val Glu Arg Ala Asp Ser Ser His Leu  
80 85 90  
Ser Ile Leu Ile Asp Pro Arg Cys Pro Asp Leu Thr Asp Ser Phe  
95 100 105

Ala Arg Leu Glu Ser	Ala Gln Ala Ser	Val Leu Gln Ala Leu Thr	110	115	120
Glu His Gln Ala Gln	Pro Arg Leu Val	Gly Asp Gln Glu Gln Glu	125	130	135
Leu Leu Asp Thr Leu	Ala Asp Gln Leu	Pro Arg Leu Leu Ala Arg	140	145	150
Ala Ser Glu Leu Gln	Thr Glu Cys Met	Gly Leu Arg Lys Gly His	155	160	165
Gly Thr Leu Gly Gln	Gly Leu Ser Ala	Leu Gln Ser Glu Gln Gly	170	175	180
Arg Leu Ile Gln Leu	Leu Ser Glu Ser	Gln Gly His Met Ala His	185	190	195
Leu Val Asn Ser Val	Ser Asp Ile Leu	Asp Ala Leu Gln Arg Asp	200	205	210
Arg Gly Leu Gly Arg	Pro Arg Asn Lys	Ala Asp Leu Gln Arg Ala	215	220	225
Pro Ala Arg Gly Thr	Arg Pro Arg Gly	Cys Ala Thr Gly Ser Arg	230	235	240
Pro Arg Asp Cys Leu	Asp Val Leu Leu	Ser Gly Gln Gln Asp Asp	245	250	255
Gly Val Tyr Ser Val	Phe Pro Thr His	Tyr Pro Ala Gly Phe Gln	260	265	270
Val Tyr Cys Asp Met	Arg Thr Asp Gly	Gly Gly Trp Thr Val Phe	275	280	285
Gln Arg Arg Glu Asp	Gly Ser Val Asn	Phe Phe Arg Gly Trp Asp	290	295	300
Ala Tyr Arg Asp Gly	Phe Gly Arg Leu	Thr Gly Glu His Trp Leu	305	310	315
Gly Leu Lys Arg Ile	His Ala Leu Thr	Thr Gln Ala Ala Tyr Glu	320	325	330
Leu His Val Asp Leu	Glu Asp Phe Glu	Asn Gly Thr Ala Tyr Ala	335	340	345
Arg Tyr Gly Ser Phe	Gly Val Gly Leu	Phe Ser Val Asp Pro Glu	350	355	360
Glu Asp Gly Tyr Pro	Leu Thr Val Ala	Asp Tyr Ser Gly Thr Ala	365	370	375
Gly Asp Ser Leu Leu	Lys His Ser Gly	Met Arg Phe Thr Thr Lys	380	385	390
Asp Arg Asp Ser Asp	His Ser Glu Asn	Asn Cys Ala Ala Phe Tyr	395	400	405
Arg Gly Ala Trp Trp	Tyr Arg Asn Cys	His Thr Ser Asn Leu Asn	410	415	420



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 aagacagcaa aagttgggag gactgtaaat atttctgcct tagtgaaaac 650  
 tctacatgac tgaagataaa caaacaagaa gacctggaat ttgccgcgtc 700  
 tcagagctac tctgagtttt tctactotta ttggacaggg cttttgcgcc 750  
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<210> 319  
 <211> 280  
 <212> PRT  
 <213> Homo sapiens



<400> 319

Met Gln Ala Lys Tyr Ser Ser Thr Arg Asp Met Leu Asp Asp Asp  
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Gly Asp Thr Thr Met Ser Leu His Ser Gln Ala Ser Ala Thr Thr  
20 25 30  
Arg His Pro Glu Pro Arg Arg Thr Glu His Arg Ala Pro Ser Ser  
35 40 45  
Thr Trp Arg Pro Val Ala Leu Thr Leu Leu Thr Leu Cys Leu Val  
50 55 60  
Leu Leu Ile Gly Leu Ala Ala Leu Gly Leu Leu Phe Phe Gln Tyr  
65 70 75  
Tyr Gln Leu Ser Asn Thr Gly Gln Asp Thr Ile Ser Gln Met Glu  
80 85 90  
Glu Arg Leu Gly Asn Thr Ser Gln Glu Leu Gln Ser Leu Gln Val  
95 100 105  
Gln Asn Ile Lys Leu Ala Gly Ser Leu Gln His Val Ala Glu Lys  
110 115 120  
Leu Cys Arg Glu Leu Tyr Asn Lys Ala Gly Ala His Arg Cys Ser  
125 130 135  
Pro Cys Thr Glu Gln Trp Lys Trp His Gly Asp Asn Cys Tyr Gln  
140 145 150  
Phe Tyr Lys Asp Ser Lys Ser Trp Glu Asp Cys Lys Tyr Phe Cys  
155 160 165  
Leu Ser Glu Asn Ser Thr Met Leu Lys Ile Asn Lys Gln Glu Asp  
170 175 180  
Leu Glu Phe Ala Ala Ser Gln Ser Tyr Ser Glu Phe Phe Tyr Ser  
185 190 195  
Tyr Trp Thr Gly Leu Leu Arg Pro Asp Ser Gly Lys Ala Trp Leu  
200 205 210  
Trp Met Asp Gly Thr Pro Phe Thr Ser Glu Leu Phe His Ile Ile  
215 220 225  
Ile Asp Val Thr Ser Pro Arg Ser Arg Asp Cys Val Ala Ile Leu  
230 235 240  
Asn Gly Met Ile Phe Ser Lys Asp Cys Lys Glu Leu Lys Arg Cys  
245 250 255  
Val Cys Glu Arg Arg Ala Gly Met Val Lys Pro Glu Ser Leu His  
260 265 270  
Val Pro Pro Glu Thr Leu Gly Glu Gly Asp  
275 280

<210> 320

<211> 468

<212> DNA

<213> Homo sapiens

<220>  
<221> unsure  
<222> 59, 95, 149, 331, 364, 438, 446  
<223> unknown base

<400> 320  
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gggacatgnt ggatgatgat gggacaccac catgagcctg cattntcaag 100  
cttttgccac aattcggcat ccagagcccc ggcgcacaga gcacagggnt 150  
cctttttcaa cgtggcgacc agtggccctg accctgctga ctttgtgctt 200  
gggtgctgctg atagggctgg cagccctggg gcttttgttt tttcagtact 250  
accagctctc caatactggt caagacacca tttctcaaat ggaagaaaga 300  
ttaggaaata cgtcccaaga gttgcaattt nttcaagtcc agaataataa 350  
gcttgcagga agtntgcagc atgtggctga aaaactctgt cgtgagctgt 400  
ataacaaagc tggaggaact ttgaaggagg gcaaagtntc ctcatntact 450  
atacacacac cacttccc 468

<210> 321  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 321  
atgcaggcca agtacagcag cac 23

<210> 322  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 322  
catgctgacg acttcctgca agc 23

<210> 323  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 323  
ccacacagtc tctgcttctt ggg 23

<210> 324  
<211> 40  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 324  
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<210> 325  
<211> 2988  
<212> DNA  
<213> Homo sapiens

<400> 325  
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gagggagcgg gcccgcgcgc ggggcccagag ccctccgat cgcgccctc 150  
cccgtccccg cccctcggga gactcctctg gctgctctgg gggttcgccg 200  
gggcccggga cccgcgggtcc gggcgccatg cgggcatcgc tgctgctgtc 250  
ggtgctgcgg cccgcagggc ccgtggccgt gggcatctcc ctgggcttca 300  
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<210> 326

<211> 775

<212> PRT

<213> Homo sapiens

<400> 326

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				20					25					30
Val	Thr	Trp	Val	Glu	Glu	Pro	Cys	Gly	Pro	Gly	Pro	Pro	Gln	Pro
				35					40					45
Gly	Asp	Ser	Glu	Leu	Pro	Pro	Arg	Gly	Asn	Thr	Asn	Ala	Ala	Arg
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Arg	Pro	Asn	Ser	Val	Gln	Pro	Gly	Ala	Glu	Arg	Glu	Lys	Pro	Gly
				65					70					75
Ala	Gly	Glu	Gly	Ala	Gly	Glu	Asn	Trp	Glu	Pro	Arg	Val	Leu	Pro
				80					85					90
Tyr	His	Pro	Ala	Gln	Pro	Gly	Gln	Ala	Ala	Lys	Lys	Ala	Val	Arg
				95					100					105
Thr	Arg	Tyr	Ile	Ser	Thr	Glu	Leu	Gly	Ile	Arg	Gln	Arg	Leu	Leu
				110					115					120
Val	Ala	Val	Leu	Thr	Ser	Gln	Thr	Thr	Leu	Pro	Thr	Leu	Gly	Val
				125					130					135
Ala	Val	Asn	Arg	Thr	Leu	Gly	His	Arg	Leu	Glu	Arg	Val	Val	Phe
				140					145					150
Leu	Thr	Gly	Ala	Arg	Gly	Arg	Arg	Ala	Pro	Pro	Gly	Met	Ala	Val
				155					160					165
Val	Thr	Leu	Gly	Glu	Glu	Arg	Pro	Ile	Gly	His	Leu	His	Leu	Ala
				170					175					180
Leu	Arg	His	Leu	Leu	Glu	Gln	His	Gly	Asp	Asp	Phe	Asp	Trp	Phe
				185					190					195
Phe	Leu	Val	Pro	Asp	Thr	Thr	Tyr	Thr	Glu	Ala	His	Gly	Leu	Ala
				200					205					210
Arg	Leu	Thr	Gly	His	Leu	Ser	Leu	Ala	Ser	Ala	Ala	His	Leu	Tyr
				215					220					225
Leu	Gly	Arg	Pro	Gln	Asp	Phe	Ile	Gly	Gly	Glu	Pro	Thr	Pro	Gly
				230					235					240
Arg	Tyr	Cys	His	Gly	Gly	Phe	Gly	Val	Leu	Leu	Ser	Arg	Met	Leu
				245					250					255
Leu	Gln	Gln	Leu	Arg	Pro	His	Leu	Glu	Gly	Cys	Arg	Asn	Asp	Ile
				260					265					270

Val Ser Ala Arg	Pro Asp Glu Trp Leu Gly Arg Cys Ile Leu Asp	275	280	285
Ala Thr Gly Val	Gly Cys Thr Gly Asp His Glu Gly Val His Tyr	290	295	300
Ser His Leu Glu	Leu Ser Pro Gly Glu Pro Val Gln Glu Gly Asp	305	310	315
Pro His Phe Arg	Ser Ala Leu Thr Ala His Pro Val Arg Asp Pro	320	325	330
Val His Met Tyr	Gln Leu His Lys Ala Phe Ala Arg Ala Glu Leu	335	340	345
Glu Arg Thr Tyr	Gln Glu Ile Gln Glu Leu Gln Trp Glu Ile Gln	350	355	360
Asn Thr Ser His	Leu Ala Val Asp Gly Asp Arg Ala Ala Ala Trp	365	370	375
Pro Val Gly Ile	Pro Ala Pro Ser Arg Pro Ala Ser Arg Phe Glu	380	385	390
Val Leu Arg Trp	Asp Tyr Phe Thr Glu Gln His Ala Phe Ser Cys	395	400	405
Ala Asp Gly Ser	Pro Arg Cys Pro Leu Arg Gly Ala Asp Arg Ala	410	415	420
Asp Val Ala Asp	Val Leu Gly Thr Ala Leu Glu Glu Leu Asn Arg	425	430	435
Arg Tyr His Pro	Ala Leu Arg Leu Gln Lys Gln Gln Leu Val Asn	440	445	450
Gly Tyr Arg Arg	Phe Asp Pro Ala Arg Gly Met Glu Tyr Thr Leu	455	460	465
Asp Leu Gln Leu	Glu Ala Leu Thr Pro Gln Gly Gly Arg Arg Pro	470	475	480
Leu Thr Arg Arg	Val Gln Leu Leu Arg Pro Leu Ser Arg Val Glu	485	490	495
Ile Leu Pro Val	Pro Tyr Val Thr Glu Ala Ser Arg Leu Thr Val	500	505	510
Leu Leu Pro Leu	Ala Ala Ala Glu Arg Asp Leu Ala Pro Gly Phe	515	520	525
Leu Glu Ala Phe	Ala Thr Ala Ala Leu Glu Pro Gly Asp Ala Ala	530	535	540
Ala Ala Leu Thr	Leu Leu Leu Leu Tyr Glu Pro Arg Gln Ala Gln	545	550	555
Arg Val Ala His	Ala Asp Val Phe Ala Pro Val Lys Ala His Val	560	565	570
Ala Glu Leu Glu	Arg Arg Phe Pro Gly Ala Arg Val Pro Trp Leu	575	580	585

Ser Val Gln Thr	Ala Ala Pro Ser Pro	Leu Arg Leu Met Asp	Leu
	590	595	600
Leu Ser Lys Lys	His Pro Leu Asp Thr	Leu Phe Leu Leu Ala	Gly
	605	610	615
Pro Asp Thr Val	Leu Thr Pro Asp Phe	Leu Asn Arg Cys Arg	Met
	620	625	630
His Ala Ile Ser	Gly Trp Gln Ala Phe	Phe Pro Met His Phe	Gln
	635	640	645
Ala Phe His Pro	Gly Val Ala Pro Pro	Gln Gly Pro Gly Pro	Pro
	650	655	660
Glu Leu Gly Arg	Asp Thr Gly Arg Phe	Asp Arg Gln Ala Ala	Ser
	665	670	675
Glu Ala Cys Phe	Tyr Asn Ser Asp Tyr	Val Ala Ala Arg Gly	Arg
	680	685	690
Leu Ala Ala Ala	Ser Glu Gln Glu Glu	Glu Leu Leu Glu Ser	Leu
	695	700	705
Asp Val Tyr Glu	Leu Phe Leu His Phe	Ser Ser Leu His Val	Leu
	710	715	720
Arg Ala Val Glu	Pro Ala Leu Leu Gln	Arg Tyr Arg Ala Gln	Thr
	725	730	735
Cys Ser Ala Arg	Leu Ser Glu Asp Leu	Tyr His Arg Cys Leu	Gln
	740	745	750
Ser Val Leu Glu	Gly Leu Gly Ser Arg	Thr Gln Leu Ala Met	Leu
	755	760	765
Leu Phe Glu Gln	Glu Gln Gly Asn Ser	Thr	
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<210> 327

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 327

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<210> 328

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 328

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<210> 329

<211> 20

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<400> 329  
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<210> 331  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 331  
atgcatggga aagaaggcct gccc 24

<210> 332  
<211> 47  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 332  
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<210> 333  
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<212> DNA  
<213> Homo sapiens

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gctcccctag tggagaaaag gagtagctat tagccaattc ggcaggggccc 150  
gcttttttaga agcttgattt cctttgaaga tgaaagacta gcggaagctc 200  
tgcctctttc ccagtgggc gagggaaactc ggggcgattg gctgggaact 250  
gtatccaccc aaatgtcacc gatttcttcc tatgcaggaa atgagcagac 300  
ccatcaataa gaaatttctc agcctggccg aaaatggttg gccccacgaa 350  
gccacgacaa ctggaggcaa agagggttgc tcaacgcccc gcctcattgg 400



aaaaccaa at cagatctggg acctatatag cgtggcggag gcggggcgat 450  
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 ctgcttcgac cccagcaaga tccagctgcc agaggatgag tgaccagttg 1000  
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<210> 334  
 <211> 153  
 <212> PRT  
 <213> Homo sapiens

<400> 334  
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 Ser Ser Phe Ser Arg Thr Val Val Ala Pro Ser Ala Val Ala Gly  
 35 40 45  
 Lys Arg Pro Pro Glu Pro Thr Thr Pro Trp Gln Glu Asp Pro Glu  
 50 55 60  
 Pro Glu Asp Glu Asn Leu Tyr Glu Lys Asn Pro Asp Ser His Gly  
 65 70 75  
 Tyr Asp Lys Asp Pro Val Leu Asp Val Trp Asn Met Arg Leu Val  
 80 85 90  
 Phe Phe Phe Gly Val Ser Ile Ile Leu Val Leu Gly Ser Thr Phe  
 95 100 105  
 Val Ala Tyr Leu Pro Asp Tyr Arg Met Lys Glu Trp Ser Arg Arg  
 110 115 120  
 Glu Ala Glu Arg Leu Val Lys Tyr Arg Glu Ala Asn Gly Leu Pro  
 125 130 135  
 Ile Met Glu Ser Asn Cys Phe Asp Pro Ser Lys Ile Gln Leu Pro  
 140 145 150

Glu Asp Glu

<210> 335  
<211> 442  
<212> DNA  
<213> Homo sapiens

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<210> 336  
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<212> DNA  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 336  
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<210> 337  
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<212> DNA  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 337  
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<212> DNA  
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<223> Synthetic oligonucleotide probe

<400> 338  
aatctagctt ctccaggact gtggctgccc cgtccgctgt 40

<210> 339  
<211> 2162  
<212> DNA

姓名	性别	年龄	籍贯	职业	文化程度	健康状况	婚姻状况	子女情况	其他
王德胜	男	45	山东	工人	小学	良好	已婚	2子1女	
李秀英	女	38	河北	农民	初中	良好	已婚	1子1女	
张国强	男	52	河南	干部	高中	良好	已婚	2子1女	
刘小红	女	28	江苏	教师	大学	良好	未婚	无	
陈为民	男	40	浙江	商人	小学	良好	已婚	1子1女	
赵大刚	男	35	湖北	工人	初中	良好	已婚	2子1女	
孙丽娟	女	32	湖南	护士	高中	良好	已婚	1子1女	
周永年	男	58	四川	退休	小学	良好	已婚	3子1女	
吴小芳	女	25	安徽	学生	大学	良好	未婚	无	
郑为民	男	42	江西	工人	初中	良好	已婚	1子1女	
徐大伟	男	30	广东	商人	小学	良好	已婚	2子1女	
黄小红	女	22	广西	学生	高中	良好	未婚	无	
周国强	男	48	福建	干部	大学	良好	已婚	1子1女	
李秀珍	女	36	山西	工人	初中	良好	已婚	2子1女	
张为民	男	55	陕西	退休	小学	良好	已婚	3子1女	
刘小红	女	29	云南	教师	高中	良好	未婚	无	
陈大刚	男	33	贵州	工人	初中	良好	已婚	1子1女	
孙丽娟	女	31	海南	护士	高中	良好	已婚	1子1女	
周永年	男	59	宁夏	退休	小学	良好	已婚	3子1女	
吴小芳	女	26	青海	学生	高中	良好	未婚	无	
郑为民	男	43	甘肃	工人	初中	良好	已婚	1子1女	
徐大伟	男	34	内蒙古	商人	小学	良好	已婚	2子1女	
黄小红	女	23	新疆	学生	高中	良好	未婚	无	
周国强	男	49	西藏	干部	大学	良好	已婚	1子1女	
李秀珍	女	37	四川	工人	初中	良好	已婚	2子1女	
张为民	男	56	重庆	退休	小学	良好	已婚	3子1女	
刘小红	女	30	湖南	教师	高中	良好	未婚	无	
陈大刚	男	34	湖北	工人	初中	良好	已婚	1子1女	
孙丽娟	女	32	江西	护士	高中	良好	已婚	1子1女	
周永年	男	60	安徽	退休	小学	良好	已婚	3子1女	
吴小芳	女	27	浙江	学生	高中	良好	未婚	无	
郑为民	男	44	江苏	工人	初中	良好	已婚	1子1女	
徐大伟	男	35	山东	商人	小学	良好	已婚	2子1女	
黄小红	女	24	河南	学生	高中	良好	未婚	无	
周国强	男	50	河北	干部	大学	良好	已婚	1子1女	
李秀珍	女	38	山西	工人	初中	良好	已婚	2子1女	
张为民	男	57	陕西	退休	小学	良好	已婚	3子1女	
刘小红	女	31	云南	教师	高中	良好	未婚	无	
陈大刚	男	35	贵州	工人	初中	良好	已婚	1子1女	
孙丽娟	女	33	海南	护士	高中	良好	已婚	1子1女	
周永年	男	61	宁夏	退休	小学	良好	已婚	3子1女	
吴小芳	女	28	青海	学生	高中	良好	未婚	无	
郑为民	男	45	甘肃	工人	初中	良好	已婚	1子1女	
徐大伟	男	36	内蒙古	商人	小学	良好	已婚	2子1女	
黄小红	女	25	新疆	学生	高中	良好	未婚	无	
周国强	男	51	西藏	干部	大学	良好	已婚	1子1女	
李秀珍	女	39	四川	工人	初中	良好	已婚	2子1女	
张为民	男	58	重庆	退休	小学	良好	已婚	3子1女	
刘小红	女	32	湖南	教师	高中	良好	未婚	无	
陈大刚	男	36	湖北	工人	初中	良好	已婚	1子1女	
孙丽娟									

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tgacttgctt	gacaccgcca	tgatcaacaa	ctctcgaaac	ctcaacatcc	1000
agctcaagtg	gaagagaccc	ccagagaaatg	aggccccccc	agtgcccttc	1050
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gagcacactg	ctgtacaaca	cccacccata	ccgggccttc	ccggtgctgc	1150
tgctggacac	cgtaccctgg	tatctgcggc	tgtatgtgca	caccctcacc	1200
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tgcccaggac	cggtgcaac	cccacctcct	ggagatgctg	attcagctgc	1300
cggccaactc	agtcaccaag	gtttccatcc	agtttgagcg	ggcgctgctg	1350
aagtggaccg	agtacacgcc	agatcctaac	catggcttct	atgtcagccc	1400
atctgtcctc	agcgcccttg	tgcccagcat	ggtagcagcc	aagccagtgg	1450
actgggaaga	gagtcccttc	ttcaacagcc	tgttccagct	ctctgatggc	1500



Ala Ser Phe Lys Pro Leu Gly Leu Ala Asn Asp Thr Asp His Tyr	155	160	165
Phe Leu Arg Tyr Ala Val Leu Pro Arg Glu Val Val Cys Thr Glu	170	175	180
Asn Leu Thr Pro Trp Lys Lys Leu Leu Pro Cys Ser Ser Lys Ala	185	190	195
Gly Leu Ser Val Leu Leu Lys Ala Asp Arg Leu Phe His Thr Ser	200	205	210
Tyr His Ser Gln Ala Val His Ile Arg Pro Val Cys Arg Asn Ala	215	220	225
Arg Cys Thr Ser Ile Ser Trp Glu Leu Arg Gln Thr Leu Ser Val	230	235	240
Val Phe Asp Ala Phe Ile Thr Gly Gln Gly Lys Lys Asp Trp Ser	245	250	255
Leu Phe Arg Met Phe Ser Arg Thr Leu Thr Glu Pro Cys Pro Leu	260	265	270
Ala Ser Glu Ser Arg Val Tyr Val Asp Ile Thr Thr Tyr Asn Gln	275	280	285
Asp Asn Glu Thr Leu Glu Val His Pro Pro Pro Thr Thr Thr Tyr	290	295	300
Gln Asp Val Ile Leu Gly Thr Arg Lys Thr Tyr Ala Ile Tyr Asp	305	310	315
Leu Leu Asp Thr Ala Met Ile Asn Asn Ser Arg Asn Leu Asn Ile	320	325	330
Gln Leu Lys Trp Lys Arg Pro Pro Glu Asn Glu Ala Pro Pro Val	335	340	345
Pro Phe Leu His Ala Gln Arg Tyr Val Ser Gly Tyr Gly Leu Gln	350	355	360
Lys Gly Glu Leu Ser Thr Leu Leu Tyr Asn Thr His Pro Tyr Arg	365	370	375
Ala Phe Pro Val Leu Leu Leu Asp Thr Val Pro Trp Tyr Leu Arg	380	385	390
Leu Tyr Val His Thr Leu Thr Ile Thr Ser Lys Gly Lys Glu Asn	395	400	405
Lys Pro Ser Tyr Ile His Tyr Gln Pro Ala Gln Asp Arg Leu Gln	410	415	420
Pro His Leu Leu Glu Met Leu Ile Gln Leu Pro Ala Asn Ser Val	425	430	435
Thr Lys Val Ser Ile Gln Phe Glu Arg Ala Leu Leu Lys Trp Thr	440	445	450
Glu Tyr Thr Pro Asp Pro Asn His Gly Phe Tyr Val Ser Pro Ser	455	460	465

Val	Leu	Ser	Ala	Leu	Val	Pro	Ser	Met	Val	Ala	Ala	Lys	Pro	Val	
				470					475					480	
Asp	Trp	Glu	Glu	Ser	Pro	Leu	Phe	Asn	Ser	Leu	Phe	Pro	Val	Ser	
				485					490					495	
Asp	Gly	Ser	Asn	Tyr	Phe	Val	Arg	Leu	Tyr	Thr	Glu	Pro	Leu	Leu	
				500					505					510	
Val	Asn	Leu	Pro	Thr	Pro	Asp	Phe	Ser	Met	Pro	Tyr	Asn	Val	Ile	
				515					520					525	
Cys	Leu	Thr	Cys	Thr	Val	Val	Ala	Val	Cys	Tyr	Gly	Ser	Phe	Tyr	
				530					535					540	
Asn	Leu	Leu	Thr	Arg	Thr	Phe	His	Ile	Glu	Glu	Pro	Arg	Thr	Gly	
				545					550					555	
Gly	Leu	Ala	Lys	Arg	Leu	Ala	Asn	Leu	Ile	Arg	Arg	Ala	Arg	Gly	
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Val Pro Pro Leu

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 <212> DNA  
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<220>  
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<210> 343  
 <211> 44  
 <212> DNA  
 <213> Artificial Sequence

<220>  
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<400> 343  
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<210> 344  
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 <212> DNA  
 <213> Homo sapiens

<400> 344

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 gtttgcccag ctgacaacgt acgctgcttc aagtccgatc ctccccagtg 150  
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 gtcagagaag agaaactggc cctcaccaga tgctgaatct gctggtgcct 700  
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<210> 345

<211> 111

<212> PRT

<213> Homo sapiens

<400> 345

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Val	Thr	Leu	Val	Ala	Val	Glu	Gly	Val	Lys	Glu	Gly	Ile	Glu	Lys
				20					25					30
Ala	Gly	Val	Cys	Pro	Ala	Asp	Asn	Val	Arg	Cys	Phe	Lys	Ser	Asp
				35					40					45
Pro	Pro	Gln	Cys	His	Thr	Asp	Gln	Asp	Cys	Leu	Gly	Glu	Arg	Lys
				50					55					60
Cys	Cys	Tyr	Leu	His	Cys	Gly	Phe	Lys	Cys	Val	Ile	Pro	Val	Lys
				65					70					75
Glu	Leu	Glu	Glu	Gly	Gly	Asn	Lys	Asp	Glu	Asp	Val	Ser	Arg	Pro
				80					85					90
Tyr	Pro	Glu	Pro	Gly	Trp	Glu	Ala	Lys	Cys	Pro	Gly	Ser	Ser	Ser
				95					100					105
Thr	Arg	Cys	Pro	Gln	Lys									
				110										

<210> 346  
 <211> 2528  
 <212> DNA  
 <213> Homo sapiens

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 gccccaggac atgcagaacc ttctctaga acccgacca ccaccatgag 150  
 gtcttgCCTG tggagatgca ggcacctgag ccaaggcgtc cagtggtcct 200  
 tgctttctggc tgtcctggtc ttctttctct tcgccttgcc ctcttttatt 250  
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 agaaaggTct ctacagtccc tggcaaagcc taagtccag gcacccacaa 350  
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 cagcactacg tgttcogatt gagcggagct ctcatCaaag gctacgaaca 1350  
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<210> 347

&lt;212&gt; PRT

<213> Homo sapiens

<400> 347

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Leu Pro Ser Phe Ile Lys Glu Pro Gln Thr Lys Pro Ser Arg His  
35 40 45

Gln Arg Thr Glu Asn Ile Lys Glu Arg Ser Leu Gln Ser Leu Ala  
50 55 60

Lys Pro Lys Ser Gln Ala Pro Thr Arg Ala Arg Arg Thr Thr Ile

	65	70	75
Tyr Ala Glu Pro	Ala 80	Pro Glu Asn Asn Ala 85	Leu Asn Thr Gln Thr 90
Gln Pro Lys Ala	His 95	Thr Thr Gly Asp Arg 100	Gly Lys Glu Ala Asn 105
Gln Ala Pro Pro	Glu 110	Glu Gln Asp Lys Val 115	Pro His Thr Ala Gln 120
Arg Ala Ala Trp	Lys 125	Ser Pro Glu Lys Glu 130	Lys Thr Met Val Asn 135
Thr Leu Ser Pro	Arg 140	Gly Gln Asp Ala Gly 145	Met Ala Ser Gly Arg 150
Thr Glu Ala Gln	Ser 155	Trp Lys Ser Gln Asp 160	Thr Lys Thr Thr Gln 165
Gly Asn Gly Gly	Gln 170	Thr Arg Lys Leu Thr 175	Ala Ser Arg Thr Val 180
Ser Glu Lys His	Gln 185	Gly Lys Ala Ala Thr 190	Thr Ala Lys Thr Leu 195
Ile Pro Lys Ser	Gln 200	His Arg Met Leu Ala 205	Pro Thr Gly Ala Val 210
Ser Thr Arg Thr	Arg 215	Gln Lys Gly Val Thr 220	Thr Ala Val Ile Pro 225
Pro Lys Glu Lys	Lys 230	Pro Gln Ala Thr Pro 235	Pro Pro Ala Pro Phe 240
Gln Ser Pro Thr	Thr 245	Gln Arg Asn Gln Arg 250	Leu Lys Ala Ala Asn 255
Phe Lys Ser Glu	Pro 260	Arg Trp Asp Phe Glu 265	Glu Lys Tyr Ser Phe 270
Glu Ile Gly Gly	Leu 275	Gln Thr Thr Cys Pro 280	Asp Ser Val Lys Ile 285
Lys Ala Ser Lys	Ser 290	Leu Trp Leu Gln Lys 295	Leu Phe Leu Pro Asn 300
Leu Thr Leu Phe	Leu 305	Asp Ser Arg His Phe 310	Asn Gln Ser Glu Trp 315
Asp Arg Leu Glu	His 320	Phe Ala Pro Pro Phe 325	Gly Phe Met Glu Leu 330
Asn Tyr Ser Leu	Val 335	Gln Lys Val Val Thr 340	Arg Phe Pro Pro Val 345
Pro Gln Gln Gln	Leu 350	Leu Leu Ala Ser Leu 355	Pro Ala Gly Ser Leu 360
Arg Cys Ile Thr	Cys 365	Ala Val Val Gly Asn 370	Gly Gly Ile Leu Asn 375
Asn Ser His Met	Gly	Gln Glu Ile Asp Ser	His Asp Tyr Val Phe

				380					385					390	
Arg	Leu	Ser	Gly	Ala 395	Leu	Ile	Lys	Gly	Tyr 400	Glu	Gln	Asp	Val	Gly 405	
Thr	Arg	Thr	Ser	Phe 410	Tyr	Gly	Phe	Thr	Ala 415	Phe	Ser	Leu	Thr	Gln 420	
Ser	Leu	Leu	Ile	Leu 425	Gly	Asn	Arg	Gly	Phe 430	Lys	Asn	Val	Pro	Leu 435	
Gly	Lys	Asp	Val	Arg 440	Tyr	Leu	His	Phe	Leu 445	Glu	Gly	Thr	Arg	Asp 450	
Tyr	Glu	Trp	Leu	Glu 455	Ala	Leu	Leu	Met	Asn 460	Gln	Thr	Val	Met	Ser 465	
Lys	Asn	Leu	Phe	Trp 470	Phe	Arg	His	Arg	Pro 475	Gln	Glu	Ala	Phe	Arg 480	
Glu	Ala	Leu	His	Met 485	Asp	Arg	Tyr	Leu	Leu 490	Leu	His	Pro	Asp	Phe 495	
Leu	Arg	Tyr	Met	Lys 500	Asn	Arg	Phe	Leu	Arg 505	Ser	Lys	Thr	Leu	Asp 510	
Gly	Ala	His	Trp	Arg 515	Ile	Tyr	Arg	Pro	Thr 520	Thr	Gly	Ala	Leu	Leu 525	
Leu	Leu	Thr	Ala	Leu 530	Gln	Leu	Cys	Asp	Gln 535	Val	Ser	Ala	Tyr	Gly 540	
Phe	Ile	Thr	Glu	Gly 545	His	Glu	Arg	Phe	Ser 550	Asp	His	Tyr	Tyr	Asp 555	
Thr	Ser	Trp	Lys	Arg 560	Leu	Ile	Phe	Tyr	Ile 565	Asn	His	Asp	Phe	Lys 570	
Leu	Glu	Arg	Glu	Val 575	Trp	Lys	Arg	Leu	His 580	Asp	Glu	Gly	Ile	Ile 585	
Arg	Leu	Tyr	Gln	Arg 590	Pro	Gly	Pro	Gly	Thr 595	Ala	Lys	Ala	Lys	Asn 600	

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<210> 348
<211> 496
<212> DNA
<213> Homo sapiens
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 tctgctgccc cttcagtgat gccaaccttg ggagatgccc tcacctctgta 750  
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 <211> 197  
 <212> PRT  
 <213> Homo sapiens

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                   20                  25                  30  
 Cys Leu Trp Tyr Leu Asp Arg Asn Gly Ser Trp His Pro Gly Phe  
                   35                  40                  45  
 Asn Cys Glu Phe Phe Thr Phe Cys Cys Gly Thr Cys Tyr His Arg  
                   50                  55                  60  
 Tyr Cys Cys Arg Asp Leu Thr Leu Leu Ile Thr Glu Arg Gln Gln  
                   65                  70                  75  
 Lys His Cys Leu Ala Phe Ser Pro Lys Thr Ile Ala Gly Ile Ala  
                   80                  85                  90  
 Ser Ala Val Ile Leu Phe Val Ala Val Val Ala Thr Thr Ile Cys  
                   95                  100                  105  
 Cys Phe Leu Cys Ser Cys Cys Tyr Leu Tyr Arg Arg Arg Gln Gln  
                   110                  115                  120  
 Leu Gln Ser Pro Phe Glu Gly Gln Glu Ile Pro Met Thr Gly Ile  
                   125                  130                  135  
 Pro Val Gln Pro Val Tyr Pro Tyr Pro Gln Asp Pro Lys Ala Gly  
                   140                  145                  150  
 Pro Ala Pro Pro Gln Pro Gly Phe Met Tyr Pro Pro Ser Gly Pro  
                   155                  160                  165  
 Ala Pro Gln Tyr Pro Leu Tyr Pro Ala Gly Pro Pro Val Tyr Asn  
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Gly Ala

<210> 352  
 <211> 3226  
 <212> DNA  
 <213> Homo sapiens

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<210> 353  
 <211> 941  
 <212> PRT  
 <213> Homo sapiens

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 35 40 45  
 Pro Phe Pro Trp Asn Lys Ile Arg Leu Pro Glu Tyr Val Ile Pro  
 50 55 60  
 Val His Tyr Asp Leu Leu Ile His Ala Asn Leu Thr Thr Leu Thr  
 65 70 75  
 Phe Trp Gly Thr Thr Lys Val Glu Ile Thr Ala Ser Gln Pro Thr  
 80 85 90  
 Ser Thr Ile Ile Leu His Ser His His Leu Gln Ile Ser Arg Ala  
 95 100 105  
 Thr Leu Arg Lys Gly Ala Gly Glu Arg Leu Ser Glu Glu Pro Leu  
 110 115 120  
 Gln Val Leu Glu His Pro Pro Gln Glu Gln Ile Ala Leu Leu Ala  
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 Pro Glu Pro Leu Leu Val Gly Leu Pro Tyr Thr Val Val Ile His  
 140 145 150  
 Tyr Ala Gly Asn Leu Ser Glu Thr Phe His Gly Phe Tyr Lys Ser  
 155 160 165  
 Thr Tyr Arg Thr Lys Glu Gly Glu Leu Arg Ile Leu Ala Ser Thr  
 170 175 180  
 Gln Phe Glu Pro Thr Ala Ala Arg Met Ala Phe Pro Cys Phe Asp  
 185 190 195  
 Glu Pro Ala Phe Lys Ala Ser Phe Ser Ile Lys Ile Arg Arg Glu  
 200 205 210  
 Pro Arg His Leu Ala Ile Ser Asn Met Pro Leu Val Lys Ser Val



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Thr Val Ala Glu Gly	Leu Ile Glu Asp	His Phe Asp Val Thr	Val		
	230	235	240		
Lys Met Ser Thr Tyr	Leu Val Ala Phe	Ile Ile Ser Asp Phe	Glu		
	245	250	255		
Ser Val Ser Lys Ile	Thr Lys Ser Gly	Val Lys Val Ser Val	Tyr		
	260	265	270		
Ala Val Pro Asp Lys	Ile Asn Gln Ala	Asp Tyr Ala Leu Asp	Ala		
	275	280	285		
Ala Val Thr Leu Leu	Glu Phe Tyr Glu	Asp Tyr Phe Ser Ile	Pro		
	290	295	300		
Tyr Pro Leu Pro Lys	Gln Asp Leu Ala	Ala Ile Pro Asp Phe	Gln		
	305	310	315		
Ser Gly Ala Met Glu	Asn Trp Gly Leu	Thr Thr Tyr Arg Glu	Ser		
	320	325	330		
Ala Leu Leu Phe Asp	Ala Glu Lys Ser	Ser Ala Ser Ser Lys	Leu		
	335	340	345		
Gly Ile Thr Val Thr	Val Ala His Glu	Leu Ala His Gln Trp	Phe		
	350	355	360		
Gly Asn Leu Val Thr	Met Glu Trp Trp	Asn Asp Leu Trp Leu	Asn		
	365	370	375		
Glu Gly Phe Ala Lys	Phe Met Glu Phe	Val Ser Val Ser Val	Thr		
	380	385	390		
His Pro Glu Leu Lys	Val Gly Asp Tyr	Phe Phe Gly Lys Cys	Phe		
	395	400	405		
Asp Ala Met Glu Val	Asp Ala Leu Asn	Ser Ser His Pro Val	Ser		
	410	415	420		
Thr Pro Val Glu Asn	Pro Ala Gln Ile	Arg Glu Met Phe Asp	Asp		
	425	430	435		
Val Ser Tyr Asp Lys	Gly Ala Cys Ile	Leu Asn Met Leu Arg	Glu		
	440	445	450		
Tyr Leu Ser Ala Asp	Ala Phe Lys Ser	Gly Ile Val Gln Tyr	Leu		
	455	460	465		
Gln Lys His Ser Tyr	Lys Asn Thr Lys	Asn Glu Asp Leu Trp	Asp		
	470	475	480		
Ser Met Ala Ser Ile	Cys Pro Thr Asp	Gly Val Lys Gly Met	Asp		
	485	490	495		
Gly Phe Cys Ser Arg	Ser Gln His Ser	Ser Ser Ser Ser His	Trp		
	500	505	510		
His Gln Glu Gly Val	Asp Val Lys Thr	Met Met Asn Thr Trp	Thr		
	515	520	525		
Leu Gln Arg Gly Phe	Pro Leu Ile Thr	Ile Thr Val Arg Gly	Arg		

				530					535					540
Asn	Val	His	Met	Lys 545	Gln	Glu	His	Tyr	Met 550	Lys	Gly	Ser	Asp	Gly 555
Ala	Pro	Asp	Thr	Gly 560	Tyr	Leu	Trp	His	Val 565	Pro	Leu	Thr	Phe	Ile 570
Thr	Ser	Lys	Ser	Asn 575	Met	Val	His	Arg	Phe 580	Leu	Leu	Lys	Thr	Lys 585
Thr	Asp	Val	Leu	Ile 590	Leu	Pro	Glu	Glu	Val 595	Glu	Trp	Ile	Lys	Phe 600
Asn	Val	Gly	Met	Asn 605	Gly	Tyr	Tyr	Ile	Val 610	His	Tyr	Glu	Asp	Asp 615
Gly	Trp	Asp	Ser	Leu 620	Thr	Gly	Leu	Leu	Lys 625	Gly	Thr	His	Thr	Ala 630
Val	Ser	Ser	Asn	Asp 635	Arg	Ala	Ser	Leu	Ile 640	Asn	Asn	Ala	Phe	Gln 645
Leu	Val	Ser	Ile	Gly 650	Lys	Leu	Ser	Ile	Glu 655	Lys	Ala	Leu	Asp	Leu 660
Ser	Leu	Tyr	Leu	Lys 665	His	Glu	Thr	Glu	Ile 670	Met	Pro	Val	Phe	Gln 675
Gly	Leu	Asn	Glu	Leu 680	Ile	Pro	Met	Tyr	Lys 685	Leu	Met	Glu	Lys	Arg 690
Asp	Met	Asn	Glu	Val 695	Glu	Thr	Gln	Phe	Lys 700	Ala	Phe	Leu	Ile	Arg 705
Leu	Leu	Arg	Asp	Leu 710	Ile	Asp	Lys	Gln	Thr 715	Trp	Thr	Asp	Glu	Gly 720
Ser	Val	Ser	Glu	Gln 725	Met	Leu	Arg	Ser	Glu 730	Leu	Leu	Leu	Leu	Ala 735
Cys	Val	His	Asn	Tyr 740	Gln	Pro	Cys	Val	Gln 745	Arg	Ala	Glu	Gly	Tyr 750
Phe	Arg	Lys	Trp	Lys 755	Glu	Ser	Asn	Gly	Asn 760	Leu	Ser	Leu	Pro	Val 765
Asp	Val	Thr	Leu	Ala 770	Val	Phe	Ala	Val	Gly 775	Ala	Gln	Ser	Thr	Glu 780
Gly	Trp	Asp	Phe	Leu 785	Tyr	Ser	Lys	Tyr	Gln 790	Phe	Ser	Leu	Ser	Ser 795
Thr	Glu	Lys	Ser	Gln 800	Ile	Glu	Phe	Ala	Leu 805	Cys	Arg	Thr	Gln	Asn 810
Lys	Glu	Lys	Leu	Gln 815	Trp	Leu	Leu	Asp	Glu 820	Ser	Phe	Lys	Gly	Asp 825
Lys	Ile	Lys	Thr	Gln 830	Glu	Phe	Pro	Gln	Ile 835	Leu	Thr	Leu	Ile	Gly 840
Arg	Asn	Pro	Val	Gly	Tyr	Pro	Leu	Ala	Trp	Gln	Phe	Leu	Arg	Lys

	845		850		855
Asn Trp Asn Lys	Leu Val Gln Lys Phe	Glu Leu Gly Ser Ser Ser			
	860		865		870
Ile Ala His Met	Val Met Gly Thr Thr	Asn Gln Phe Ser Thr Arg			
	875		880		885
Thr Arg Leu Glu	Glu Val Lys Gly Phe	Phe Ser Ser Leu Lys Glu			
	890		895		900
Asn Gly Ser Gln	Leu Arg Cys Val Gln	Gln Thr Ile Glu Thr Ile			
	905		910		915
Glu Glu Asn Ile	Gly Trp Met Asp Lys	Asn Phe Asp Lys Ile Arg			
	920		925		930
Val Trp Leu Gln	Ser Glu Lys Leu Glu	Arg Met			
	935		940		

<210> 354  
 <211> 1587  
 <212> DNA  
 <213> Homo sapiens

<400> 354  
 cagccacaga cgggtcatga ggcggtatt actgctggcc ctctgggggt 50  
 tcctcctccc actgccagga gtgcaggcgc tgctctgcca gtttgggaca 100  
 gttcagcatg tgtggaaggt gtccgacctt ccccggaat ggaccctaa 150  
 gaacaccagc tgcgacagcg gcttgggggtg ccaggacacg ttgatgctca 200  
 ttgagagcgg accccaagtg agcctggtgc tctccaaggg ctgcacggag 250  
 gccaaggacc aggagccccg cgctactgag caccggatgg gcccggcct 300  
 ctccctgatc tctacacct tcgtgtgccc ccaggaggac ttctgcaaca 350  
 acctcgtaa ctccctcccg ctttggggccc cacagcccc agcagacca 400  
 ggatccttga ggtgcccagt ctgcttgtct atggaaggct gtctggaggg 450  
 gacaacagaa gagatctgcc ccaaggggac cacacactgt tatgatggcc 500  
 tcctcaggct caggggagga ggcattctct ccaatctgag agtccaggga 550  
 tgcattcccc agccagggtg caacctgctc aatgggacac aggaaattgg 600  
 gcccgtgggt atgactgaga actgcaatag gaaagatttt ctgacctgtc 650  
 atcgggggac caccattatg acacacggaa acttgggtca agaaccact 700  
 gattggacca catcgaatac cgagatgtgc gaggtggggc aggtgtgtca 750  
 ggagacgctg ctgctcatag atgtaggact cacatcaacc ctggtgggga 800  
 caaaaggctg cagcactgtt ggggtcaaaa attcccagaa gaccaccatc 850  
 cactcagccc ctctgggggt gcttgtggcc tcctataccc acttctgctc 900  
 ctcggaacctg tgcaatagtg ccagcagcag cagcgttctg ctgaactccc 950

tccctcctca agctgcccct gtcccaggag accggcagtg tcctacctgt 1000  
 gtgcagcccc ttggaacctg ttcaagtggc tccccccgaa tgacctgcc 1050  
 caggggagcc actcattgtt atgatgggta cattcatctc tcaggagggtg 1100  
 ggctgtccac caaaatgagc attcagggtt gcgtggccca accttccagc 1150  
 ttcttggtga accacaccag acaaatcggg atcttctctg cgcgtgagaa 1200  
 gcgtgatgtg cagcctcctg cctctcagca tgaggagggt ggggctgagg 1250  
 gcctggagtc tctcacttgg ggggtggggc tggcactggc cccagcgtg 1300  
 tgggtggggag tggtttgccc ttctgtctaa ctctattacc cccacgattc 1350  
 ttcacgctg ctgaccaccc aactcaacc tccctctgac ctcataacct 1400  
 aatggccttg gacaccagat tctttcccat tctgtccatg aatcatcttc 1450  
 cccacacaca atcattcata tctactcacc taacagcaac actggggaga 1500  
 gcctggagca tccggacttg ccctatggga gaggggacgc tggaggagtg 1550  
 gctgcatgta tctgataata cagaccctgt cctttca 1587

<210> 355  
 <211> 437  
 <212> PRT  
 <213> Homo sapiens

<400> 355  
 Met Ser Ala Val Leu Leu Leu Ala Leu Leu Gly Phe Ile Leu Pro  
 1 5 10 15  
 Leu Pro Gly Val Gln Ala Leu Leu Cys Gln Phe Gly Thr Val Gln  
 20 25 30  
 His Val Trp Lys Val Ser Asp Leu Pro Arg Gln Trp Thr Pro Lys  
 35 40 45  
 Asn Thr Ser Cys Asp Ser Gly Leu Gly Cys Gln Asp Thr Leu Met  
 50 55 60  
 Leu Ile Glu Ser Gly Pro Gln Val Ser Leu Val Leu Ser Lys Gly  
 65 70 75  
 Cys Thr Glu Ala Lys Asp Gln Glu Pro Arg Val Thr Glu His Arg  
 80 85 90  
 Met Gly Pro Gly Leu Ser Leu Ile Ser Tyr Thr Phe Val Cys Arg  
 95 100 105  
 Gln Glu Asp Phe Cys Asn Asn Leu Val Asn Ser Leu Pro Leu Trp  
 110 115 120  
 Ala Pro Gln Pro Pro Ala Asp Pro Gly Ser Leu Arg Cys Pro Val  
 125 130 135  
 Cys Leu Ser Met Glu Gly Cys Leu Glu Gly Thr Thr Glu Glu Ile  
 140 145 150  
 Cys Pro Lys Gly Thr Thr His Cys Tyr Asp Gly Leu Leu Arg Leu

0599752525660  
TOSTT 11501

155	160	165
Arg Gly Gly Gly Ile Phe Ser Asn Leu	Arg Val Gln Gly Cys Met	
170	175	180
Pro Gln Pro Gly Cys Asn Leu Leu Asn	Gly Thr Gln Glu Ile Gly	
185	190	195
Pro Val Gly Met Thr Glu Asn Cys Asn	Arg Lys Asp Phe Leu Thr	
200	205	210
Cys His Arg Gly Thr Thr Ile Met Thr	His Gly Asn Leu Ala Gln	
215	220	225
Glu Pro Thr Asp Trp Thr Thr Ser Asn	Thr Glu Met Cys Glu Val	
230	235	240
Gly Gln Val Cys Gln Glu Thr Leu Leu	Leu Ile Asp Val Gly Leu	
245	250	255
Thr Ser Thr Leu Val Gly Thr Lys Gly	Cys Ser Thr Val Gly Ala	
260	265	270
Gln Asn Ser Gln Lys Thr Thr Ile His	Ser Ala Pro Pro Gly Val	
275	280	285
Leu Val Ala Ser Tyr Thr His Phe Cys	Ser Ser Asp Leu Cys Asn	
290	295	300
Ser Ala Ser Ser Ser Ser Val Leu Leu	Asn Ser Leu Pro Pro Gln	
305	310	315
Ala Ala Pro Val Pro Gly Asp Arg Gln	Cys Pro Thr Cys Val Gln	
320	325	330
Pro Leu Gly Thr Cys Ser Ser Gly Ser	Pro Arg Met Thr Cys Pro	
335	340	345
Arg Gly Ala Thr His Cys Tyr Asp Gly	Tyr Ile His Leu Ser Gly	
350	355	360
Gly Gly Leu Ser Thr Lys Met Ser Ile	Gln Gly Cys Val Ala Gln	
365	370	375
Pro Ser Ser Phe Leu Leu Asn His Thr	Arg Gln Ile Gly Ile Phe	
380	385	390
Ser Ala Arg Glu Lys Arg Asp Val Gln	Pro Pro Ala Ser Gln His	
395	400	405
Glu Gly Gly Gly Ala Glu Gly Leu Glu	Ser Leu Thr Trp Gly Val	
410	415	420
Gly Leu Ala Leu Ala Pro Ala Leu Trp	Trp Gly Val Val Cys Pro	
425	430	435

Ser Cys

<210> 356  
 <211> 1238  
 <212> DNA  
 <213> Homo sapiens

<400> 356  
 gcgacgggca ggacgccccg ttgcgctagc gcggtgctcag gagttggtgt 50  
 cctgcctgcg ctcaggatga gggggaatct ggccctggtg ggcgttctaa 100  
 tcagcctggc cttcctgtca ctgctgccat ctggacatcc tcagccggct 150  
 ggcgatgacg cctgctctgt gcagatcctc gtccctggcc tcaaagggga 200  
 tgcgggagag aaggagaca aaggcgcccc cgacggcct ggaagagtcg 250  
 gccccacggg agaaaaagga gacatggggg acaaaggaca gaaaggcagt 300  
 gtgggtcgtc atggaaaaat tggcccatt ggctctaaag gtgagaaagg 350  
 agattccggt gacataggac cccctggtcc taatggagaa ccaggcctcc 400  
 catgtgagtg cagccagctg cgcaaggcca tcggggagat ggacaaccag 450  
 gtctctcagc tgaccagcga gctcaagttc atcaagaatg ctgtcgccgg 500  
 tgtgcgcgag acggagagca agatctacct gctggtgaag gaggagaagc 550  
 gctacgcgga cgcccagctg tcctgccagg gccgcggggg cagctgagc 600  
 atgccaagg acgaggctgc caatggcctg atggccgcat acctggcgca 650  
 agccggcctg gcccggtgtc tcatcgcat caacgacctg gagaaggagg 700  
 gcgccttcgt gtactctgac cactccccc tgccgacctt caacaagtgg 750  
 cgcagcgggtg agcccaacaa tgcctacgac gaggaggact gcgtggagat 800  
 ggtggcctcg ggcggctgga acgacgtggc ctgccacacc accatgtact 850  
 tcatgtgtga gtttgacaag gagaacatgt gaggctcagg ctggggctgc 900  
 ccattggggg ccccatatgt ccctgcaggg ttggcaggga cagagcccag 950  
 accatggtgc cagccaggga gctgtccctc tgtgaagggt ggaggctcac 1000  
 tgagtagagg gctgttgtct aaactgagaa aatggcctat gcttaagagg 1050  
 aaaatgaaag tgttcctggg gtgctgtctc tgaagaagca gagtttcatt 1100  
 acctgtattg tagcccaat gtcattatgt aattattacc cagaattgct 1150  
 cttccataaa gcttgtgcct ttgtccaagc tatacaataa aatctttaag 1200  
 tagtgcagta gttaagtcca aaaaaaaaaa aaaaaaaaa 1238

<210> 357  
 <211> 271  
 <212> PRT  
 <213> Homo sapiens

<400> 357  
 Met Arg Gly Asn Leu Ala Leu Val Gly Val Leu Ile Ser Leu Ala  
 1 5 10 15  
 Phe Leu Ser Leu Leu Pro Ser Gly His Pro Gln Pro Ala Gly Asp  
 20 25 30

Asp	Ala	Cys	Ser	Val	Gln	Ile	Leu	Val	Pro	Gly	Leu	Lys	Gly	Asp	35	40	45
Ala	Gly	Glu	Lys	Gly	Asp	Lys	Gly	Ala	Pro	Gly	Arg	Pro	Gly	Arg	50	55	60
Val	Gly	Pro	Thr	Gly	Glu	Lys	Gly	Asp	Met	Gly	Asp	Lys	Gly	Gln	65	70	75
Lys	Gly	Ser	Val	Gly	Arg	His	Gly	Lys	Ile	Gly	Pro	Ile	Gly	Ser	80	85	90
Lys	Gly	Glu	Lys	Gly	Asp	Ser	Gly	Asp	Ile	Gly	Pro	Pro	Gly	Pro	95	100	105
Asn	Gly	Glu	Pro	Gly	Leu	Pro	Cys	Glu	Cys	Ser	Gln	Leu	Arg	Lys	110	115	120
Ala	Ile	Gly	Glu	Met	Asp	Asn	Gln	Val	Ser	Gln	Leu	Thr	Ser	Glu	125	130	135
Leu	Lys	Phe	Ile	Lys	Asn	Ala	Val	Ala	Gly	Val	Arg	Glu	Thr	Glu	140	145	150
Ser	Lys	Ile	Tyr	Leu	Leu	Val	Lys	Glu	Glu	Lys	Arg	Tyr	Ala	Asp	155	160	165
Ala	Gln	Leu	Ser	Cys	Gln	Gly	Arg	Gly	Gly	Thr	Leu	Ser	Met	Pro	170	175	180
Lys	Asp	Glu	Ala	Ala	Asn	Gly	Leu	Met	Ala	Ala	Tyr	Leu	Ala	Gln	185	190	195
Ala	Gly	Leu	Ala	Arg	Val	Phe	Ile	Gly	Ile	Asn	Asp	Leu	Glu	Lys	200	205	210
Glu	Gly	Ala	Phe	Val	Tyr	Ser	Asp	His	Ser	Pro	Met	Arg	Thr	Phe	215	220	225
Asn	Lys	Trp	Arg	Ser	Gly	Glu	Pro	Asn	Asn	Ala	Tyr	Asp	Glu	Glu	230	235	240
Asp	Cys	Val	Glu	Met	Val	Ala	Ser	Gly	Gly	Trp	Asn	Asp	Val	Ala	245	250	255
Cys	His	Thr	Thr	Met	Tyr	Phe	Met	Cys	Glu	Phe	Asp	Lys	Glu	Asn	260	265	270

Met

<210> 358  
 <211> 972  
 <212> DNA  
 <213> Homo sapiens

<400> 358  
 agtgactgca gccttcctag atcccctcca ctcggtttct ctctttgcag 50  
 gagcaccggc agcaccagtg tgtgagggga gcaggcagcg gtcctagcca 100  
 gttccttgat cctgccagac caccagccc ccggcacaga gctgctccac 150

aggcaccatg aggatcatgc tgctattcac agccatcctg gccttcagcc 200  
 tagctcagag ctttggggct gtctgtaagg agccacagga ggaggtggtt 250  
 cctggcgggg gccgcagcaa gagggatcca gatctctacc agctgctcca 300  
 gagactcttc aaaagccact catctctgga gggattgctc aaagccctga 350  
 gccaggctag cacagatcct aaggaatcaa catctccoga gaaacgtgac 400  
 atgcatgact tctttgtggg acttatgggc aagaggagcg tccagccaga 450  
 gggaaagaca ggacctttct taccttcagt gagggttcct cggccccttc 500  
 atcccaatca gcttggatcc acaggaaagt cttccctggg aacagaggag 550  
 cagagacctt tataagactc tcctacggat gtgaatcaag agaacgtccc 600  
 cagctttggc atcctcaagt atcccccgag agcagaatag gtactccact 650  
 tccggactcc tggactgcat taggaagacc tctttccctg tcccaatccc 700  
 caggtgcgca cgctcctgtt accctttctc ttccctgttc ttgtaacatt 750  
 cttgtgcttt gactccttct ccatcttttc tacctgacct tgggtgtggaa 800  
 actgcatagt gaatatcccc aacccaatg ggcattgact gtagaatacc 850  
 ctagagtcc tgtagtgtcc tacattaaaa atataatgtc tctctctatt 900  
 cctcaacaat aaaggatttt tgcataatgaa aaaaaaaaaa aaaaaaaaaa 950  
 aaaaaaaaaa aaaaaaaaaa aa 972

<210> 359  
 <211> 135  
 <212> PRT  
 <213> Homo sapiens

<400> 359  
 Met Arg Ile Met Leu Leu Phe Thr Ala Ile Leu Ala Phe Ser Leu  
 1 5 10 15  
 Ala Gln Ser Phe Gly Ala Val Cys Lys Glu Pro Gln Glu Glu Val  
 20 25 30  
 Val Pro Gly Gly Gly Arg Ser Lys Arg Asp Pro Asp Leu Tyr Gln  
 35 40 45  
 Leu Leu Gln Arg Leu Phe Lys Ser His Ser Ser Leu Glu Gly Leu  
 50 55 60  
 Leu Lys Ala Leu Ser Gln Ala Ser Thr Asp Pro Lys Glu Ser Thr  
 65 70 75  
 Ser Pro Glu Lys Arg Asp Met His Asp Phe Phe Val Gly Leu Met  
 80 85 90  
 Gly Lys Arg Ser Val Gln Pro Glu Gly Lys Thr Gly Pro Phe Leu  
 95 100 105  
 Pro Ser Val Arg Val Pro Arg Pro Leu His Pro Asn Gln Leu Gly  
 110 115 120



Ser Thr Gly Lys Ser Ser Leu Gly Thr Glu Glu Gln Arg Pro Leu  
125 130 135

<210> 360  
<211> 1738  
<212> DNA  
<213> Homo sapiens

<400> 360  
gggcgtctcc ggctgctcct attgagctgt ctgctcgtg tgcccgtgt 50  
gcctgctgtg ccgcgctgt cgccgctgt accgcgtctg ctggacgcgg 100  
gagacgccag cgagctggtg attggagccc tgcggagagc tcaagcggcc 150  
agctctgccc caggagccca ggctgccccg tgagtcccat agttgctgca 200  
ggagtggagc catgagctgc gtccctgggtg gtgtcatccc cttggggctg 250  
ctgttcctgg tctgcggatc ccaaggctac ctccctgcca acgtcactct 300  
cttagaggag ctgctcagca aataccagca caacgagtct cactcccggg 350  
tccgcagagc catccccagg gaggacaagg aggagatcct catgctgcac 400  
aacaagcttc ggggccaggt gcagcctcag gcctccaaca tggagtacat 450  
ggtgagcgcc ggctccggcc gcagaggctg gcaccggggg tggggcctgg 500  
gccaccagcc tgctctgttc ccagccagc tctgttcccc agccagtgcg 550  
tgtgatggct ggctcagggt ctccctctggc aggggaggat cccggctctg 600  
ttctgttttg tttgtttgtt ttgagacagg gtctcactct gccactgacg 650  
ctggagtgca atggcacaat cgtcatgccc tgaaacctta gactcccggg 700  
gttaagogat cctgcttcag cctcccaagt agctggaact acaggcatgc 750  
accatggtgc ccagctagat tttaaattt ttgtggagat gggggctctg 800  
ctacgttgcc caggctggtc ttgaactcct aggetcaagc aatcctcctg 850  
cctcagcctc tcaaagtgc aggattatag gcatgagtca cctgtctctg 900  
ctctggctct gttcttaaca ttctgcaaaa acaacacaag tgggttccct 950  
gtgcagagcc tgccctggtg cttcatgtc actcttggtg gctocactgg 1000  
gaacacagct ctcagccttt ccacactgga ggcagagtgg ggagggggcc 1050  
agggtgggc tttgctgatg ctgatctcag ctgtgccaca cgctagctgc 1100  
accaccctga cttctcctta gcccggtgta gcctcacttt ccacttgag 1150  
agtccttcct cgcgtggtg ccatgactgt gagataagtc gaggtgtgta 1200  
agggcccgcc acagactgac ctgcctcccc aaccctagg ctttgctaac 1250  
cgggaaagga gctaacggtg acagaagaca gccaaagtca accctcccgg 1300  
gtgattgtga tgggtgttcc aggtgtggtt gggcgatgct gctacttgac 1350

cccaagctcc agtgtggaaa cttccttcct ggctggtttt ccagaactac 1400  
 agaggaatgg accacagtct tccaggggcc ctcctcgtcc accaaccggg 1450  
 agcctccacc ttggccatcc gtcagctatg aatggctttt taaacaaacc 1500  
 cacgtcccag cctgggtaac atggtaaagc cccgtctcta caaaaaaatc 1550  
 caagttagcc gggcatgggtg gtgcgcacct gtagtcccag ctgcagtggg 1600  
 actgaggtgg aggtggaggt ggggggtggg agctgaggaa ggaggatcgc 1650  
 ttgagcctgg gaagtcgagg ctgcagttag ctgagattgc accactgcac 1700  
 tccagcctgg gtgacagagc aagaccctgt ctcaaaaa 1738

<210> 361  
 <211> 159  
 <212> PRT  
 <213> Homo sapiens

<400> 361  
 Met Ser Cys Val Leu Gly Gly Val Ile Pro Leu Gly Leu Leu Phe  
 1 5 10 15  
 Leu Val Cys Gly Ser Gln Gly Tyr Leu Leu Pro Asn Val Thr Leu  
 20 25 30  
 Leu Glu Glu Leu Leu Ser Lys Tyr Gln His Asn Glu Ser His Ser  
 35 40 45  
 Arg Val Arg Arg Ala Ile Pro Arg Glu Asp Lys Glu Glu Ile Leu  
 50 55 60  
 Met Leu His Asn Lys Leu Arg Gly Gln Val Gln Pro Gln Ala Ser  
 65 70 75  
 Asn Met Glu Tyr Met Val Ser Ala Gly Ser Gly Arg Arg Gly Trp  
 80 85 90  
 His Arg Gly Trp Gly Leu Gly His Gln Pro Ala Leu Phe Pro Ser  
 95 100 105  
 Gln Leu Cys Ser Pro Ala Ser Ala Cys Asp Gly Trp Leu Arg Val  
 110 115 120  
 Ser Ser Gly Arg Gly Gly Ser Arg Leu Cys Ser Val Leu Phe Val  
 125 130 135  
 Cys Phe Glu Thr Gly Ser His Ser Ala Thr Asp Ala Gly Val Gln  
 140 145 150  
 Trp His Asn Arg His Ala Leu Lys Pro  
 155

<210> 362  
 <211> 422  
 <212> DNA  
 <213> Homo sapiens

<400> 362  
 aaggagaggc caccgggact tcagtgtctc ctccatccca ggagcgcagt 50

ggccactatg ggggtctgggc tgcccccttgt cctcctcttg accctccttg 100  
gcagctcaca tggaacaggg ccgggtatga ctttgcaact gaagctgaag 150  
gagtcttttc tgacaaattc ctocctatgag tccagcttcc tggaattgct 200  
tgaaaagctc tgccctcctcc tccatctccc ttcagggacc agcgtcaccc 250  
tccaccatgc aagatctcaa caccatgttg tctgcaacac atgacagcca 300  
ttgaagcctg tgtccttctt ggcccgggct tttgggcccgg ggatgcagga 350  
ggcaggcccc gaccctgtct ttcagcaggc cccaccctc ctgagtggca 400  
ataaataaaa ttcggtatgc tg 422

<210> 363  
<211> 78  
<212> PRT  
<213> Homo sapiens

<400> 363  
Met Gly Ser Gly Leu Pro Leu Val Leu Leu Leu Thr Leu Leu Gly  
1 5 10 15  
Ser Ser His Gly Thr Gly Pro Gly Met Thr Leu Gln Leu Lys Leu  
20 25 30  
Lys Glu Ser Phe Leu Thr Asn Ser Ser Tyr Glu Ser Ser Phe Leu  
35 40 45  
Glu Leu Leu Glu Lys Leu Cys Leu Leu Leu His Leu Pro Ser Gly  
50 55 60  
Thr Ser Val Thr Leu His His Ala Arg Ser Gln His His Val Val  
65 70 75  
Cys Asn Thr

<210> 364  
<211> 826  
<212> DNA  
<213> Homo sapiens

<400> 364  
aattgtatct gtgtaatgtt aaaacaaacg aaataaaata gaaggaaaaa 50  
ctttctgagt ttcaaaaaca acagactagt actctaaaga actctttaaa 100  
acaattaact gttaggattg cagttatgat tggatattat ttaattctgt 150  
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aaaaggcatg tattttaaatac tgtatgattc tcaaccatct ttagttggga 400  
aaggtccttg aaagccaatg gaaatacttt ttttttttct tggcactaat 450

caagtgagtg ttaccttttc acttagtagg atgtgttggt acgctagtaa 500  
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tacttagata tgctttctag ttgcattttc tcagcctatg taagactact 700  
ttgttgtaat agcctttgaa atttacagta ctgtctctct actatcttca 750  
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<210> 365

<400> 365

<210> 366

<400> 366



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<210> 367

<211> 402

<212> PRT

<213> Homo sapiens

<400> 367

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Met	Val	His	Tyr	Ile	Tyr	Gln	Arg	Phe	Arg	Val	Leu	Glu	Gln	Gly	35	40	45	
Leu	Glu	Lys	Cys	Thr	Gln	Ala	Thr	Arg	Ala	Tyr	Ile	Gln	Glu	Phe	50	55	60	
Gln	Glu	Phe	Ser	Lys	Asn	Ile	Ser	Val	Met	Leu	Gly	Arg	Cys	Gln	65	70	75	
Thr	Tyr	Thr	Ser	Glu	Tyr	Lys	Ser	Ala	Val	Gly	Asn	Leu	Ala	Leu	80	85	90	
Arg	Val	Glu	Arg	Ala	Gln	Arg	Glu	Ile	Asp	Tyr	Ile	Gln	Tyr	Leu	95	100	105	
Arg	Glu	Ala	Asp	Glu	Cys	Ile	Val	Ser	Glu	Asp	Lys	Thr	Leu	Ala	110	115	120	
Glu	Met	Leu	Leu	Gln	Glu	Ala	Glu	Glu	Glu	Lys	Lys	Ile	Arg	Thr	125	130	135	
Leu	Leu	Asn	Ala	Ser	Cys	Asp	Asn	Met	Leu	Met	Gly	Ile	Lys	Ser	140	145	150	
Leu	Lys	Ile	Val	Lys	Lys	Met	Met	Asp	Thr	His	Gly	Ser	Trp	Met	155	160	165	
Lys	Asp	Ala	Val	Tyr	Asn	Ser	Pro	Lys	Val	Tyr	Leu	Leu	Ile	Gly	170	175	180	
Ser	Arg	Asn	Asn	Thr	Val	Trp	Glu	Phe	Ala	Asn	Ile	Arg	Ala	Phe	185	190	195	
Met	Glu	Asp	Asn	Thr	Lys	Pro	Ala	Pro	Arg	Lys	Gln	Ile	Leu	Thr	200	205	210	

Leu	Ser	Trp	Gln	Gly	Thr	Gly	Gln	Val	Ile	Tyr	Lys	Gly	Phe	Leu	
				215					220					225	
Phe	Phe	His	Asn	Gln	Ala	Thr	Ser	Asn	Glu	Ile	Ile	Lys	Tyr	Asn	
				230					235					240	
Leu	Gln	Lys	Arg	Thr	Val	Glu	Asp	Arg	Met	Leu	Leu	Pro	Gly	Gly	
				245					250					255	
Val	Gly	Arg	Ala	Leu	Val	Tyr	Gln	His	Ser	Pro	Ser	Thr	Tyr	Ile	
				260					265					270	
Asp	Leu	Ala	Val	Asp	Glu	His	Gly	Leu	Trp	Ala	Ile	His	Ser	Gly	
				275					280					285	
Pro	Gly	Thr	His	Ser	His	Leu	Val	Leu	Thr	Lys	Ile	Glu	Pro	Gly	
				290					295					300	
Thr	Leu	Gly	Val	Glu	His	Ser	Trp	Asp	Thr	Pro	Cys	Arg	Ser	Gln	
				305					310					315	
Asp	Ala	Glu	Ala	Ser	Phe	Leu	Leu	Cys	Gly	Val	Leu	Tyr	Val	Val	
				320					325					330	
Tyr	Ser	Thr	Gly	Gly	Gln	Gly	Pro	His	Arg	Ile	Thr	Cys	Ile	Tyr	
				335					340					345	
Asp	Pro	Leu	Gly	Thr	Ile	Ser	Glu	Glu	Asp	Leu	Pro	Asn	Leu	Phe	
				350					355					360	
Phe	Pro	Lys	Arg	Pro	Arg	Ser	His	Ser	Met	Ile	His	Tyr	Asn	Pro	
				365					370					375	
Arg	Asp	Lys	Gln	Leu	Tyr	Ala	Trp	Asn	Glu	Gly	Asn	Gln	Ile	Ile	
				380					385					390	
Tyr	Lys	Leu	Gln	Thr	Lys	Arg	Lys	Leu	Pro	Leu	Lys				
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 <211> 2281  
 <212> DNA  
 <213> Homo sapiens

<400> 368  
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 ctggccctga tggcgacggc ggcggttagcg cgggggtggc tgcgcgcggg 150  
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 aaggagaagc ctcaacaaca caacttcacc caccgcctcc tggctgcagc 300  
 tctgaagagc cacagcggga acatatcttg catggacttt agcagcaatg 350  
 gcaaatacct ggctacctgt gcagatgatc gcaccatccg catctggagc 400  
 accaaggact tcctgcagcg agagcaccgc agcatgagag ccaacgtgga 450

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gagcgggtcc atggcgagtg tatcgccaac ttgtcctttg acatcactgg 1200  
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<210> 369

<211> 447

<212> PRT

<213> Homo sapiens

<400> 369

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Trp	Leu	Arg	Ala	Gly	Glu	Glu	Arg	Ser	Gly	Arg	Pro	Ala	Cys	Gln	35	40	45	
Lys	Ala	Asn	Gly	Phe	Pro	Pro	Asp	Lys	Ser	Ser	Gly	Ser	Lys	Lys	50	55	60	
Gln	Lys	Gln	Tyr	Gln	Arg	Ile	Arg	Lys	Glu	Lys	Pro	Gln	Gln	His	65	70	75	
Asn	Phe	Thr	His	Arg	Leu	Leu	Ala	Ala	Ala	Leu	Lys	Ser	His	Ser	80	85	90	
Gly	Asn	Ile	Ser	Cys	Met	Asp	Phe	Ser	Ser	Asn	Gly	Lys	Tyr	Leu	95	100	105	
Ala	Thr	Cys	Ala	Asp	Asp	Arg	Thr	Ile	Arg	Ile	Trp	Ser	Thr	Lys	110	115	120	
Asp	Phe	Leu	Gln	Arg	Glu	His	Arg	Ser	Met	Arg	Ala	Asn	Val	Glu	125	130	135	
Leu	Asp	His	Ala	Thr	Leu	Val	Arg	Phe	Ser	Pro	Asp	Cys	Arg	Ala	140	145	150	
Phe	Ile	Val	Trp	Leu	Ala	Asn	Gly	Asp	Thr	Leu	Arg	Val	Phe	Lys	155	160	165	
Met	Thr	Lys	Arg	Glu	Asp	Gly	Gly	Tyr	Thr	Phe	Thr	Ala	Thr	Pro	170	175	180	
Glu	Asp	Phe	Pro	Lys	Lys	His	Lys	Ala	Pro	Val	Ile	Asp	Ile	Gly	185	190	195	
Ile	Ala	Asn	Thr	Gly	Lys	Phe	Ile	Met	Thr	Ala	Ser	Ser	Asp	Thr	200	205	210	
Thr	Val	Leu	Ile	Trp	Ser	Leu	Lys	Gly	Gln	Val	Leu	Ser	Thr	Ile	215	220	225	
Asn	Thr	Asn	Gln	Met	Asn	Asn	Thr	His	Ala	Ala	Val	Ser	Pro	Cys	230	235	240	

Gly	Arg	Phe	Val	Ala	Ser	Cys	Gly	Phe	Thr	Pro	Asp	Val	Lys	Val	
				245					250					255	
Trp	Glu	Val	Cys	Phe	Gly	Lys	Lys	Gly	Glu	Phe	Gln	Glu	Val	Val	
				260					265					270	
Arg	Ala	Phe	Glu	Leu	Lys	Gly	His	Ser	Ala	Ala	Val	His	Ser	Phe	
				275					280					285	
Ala	Phe	Ser	Asn	Asp	Ser	Arg	Arg	Met	Ala	Ser	Val	Ser	Lys	Asp	
				290					295					300	
Gly	Thr	Trp	Lys	Leu	Trp	Asp	Thr	Asp	Val	Glu	Tyr	Lys	Lys	Lys	
				305					310					315	
Gln	Asp	Pro	Tyr	Leu	Leu	Lys	Thr	Gly	Arg	Phe	Glu	Glu	Ala	Ala	
				320					325					330	
Gly	Ala	Ala	Pro	Cys	Arg	Leu	Ala	Leu	Ser	Pro	Asn	Ala	Gln	Val	
				335					340					345	
Leu	Ala	Leu	Ala	Ser	Gly	Ser	Ser	Ile	His	Leu	Tyr	Asn	Thr	Arg	
				350					355					360	
Arg	Gly	Glu	Lys	Glu	Glu	Cys	Phe	Glu	Arg	Val	His	Gly	Glu	Cys	
				365					370					375	
Ile	Ala	Asn	Leu	Ser	Phe	Asp	Ile	Thr	Gly	Arg	Phe	Leu	Ala	Ser	
				380					385					390	
Cys	Gly	Asp	Arg	Ala	Val	Arg	Leu	Phe	His	Asn	Thr	Pro	Gly	His	
				395					400					405	
Arg	Ala	Met	Val	Glu	Glu	Met	Gln	Gly	His	Leu	Lys	Arg	Ala	Ser	
				410					415					420	
Asn	Glu	Ser	Thr	Arg	Gln	Arg	Leu	Gln	Gln	Gln	Leu	Thr	Gln	Ala	
				425					430					435	
Gln	Glu	Thr	Leu	Lys	Ser	Leu	Gly	Ala	Leu	Lys	Lys				
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 <211> 1415  
 <212> DNA  
 <213> Homo sapiens

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 gtgatcacag gggcctgtga gcgggatgtc cagtgtgggg caggcacctg 200  
 ctgtgccatc agcctgtggc ttcgagggct gcggatgtgc accccgctgg 250  
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 ccagtcccta cactgactac cctgatctct cttgtctagt acgcacatat 550  
 gcacacaggc agacatacct cccatcatga catgggtcccc aggctggcct 600  
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 aatcagcccc ctgaagactc tgggtcccagt cagcctgtgg cttgtggcct 1050  
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 ctgagagcag gttgggtgact ttgaggaggg cagtcctctg tccagattgg 1300  
 ggtgggagca agggacaggg agcagggcag gggctgaaag gggcactgat 1350  
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<210> 371

<211> 105

<212> PRT

<213> Homo sapiens

<400> 371

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Val	Ser	Asp	Cys	Ala	Val	Ile	Thr	Gly	Ala	Cys	Glu	Arg	Asp	Val
				20					25					30

Gln	Cys	Gly	Ala	Gly	Thr	Cys	Cys	Ala	Ile	Ser	Leu	Trp	Leu	Arg
				35					40					45

Gly	Leu	Arg	Met	Cys	Thr	Pro	Leu	Gly	Arg	Glu	Gly	Glu	Glu	Cys
				50					55					60

His	Pro	Gly	Ser	His	Lys	Val	Pro	Phe	Phe	Arg	Lys	Arg	Lys	His
				65					70					75

His Thr Cys Pro Cys Leu Pro Asn Leu Leu Cys Ser Arg Phe Pro  
80 85 90

Asp Gly Arg Tyr Arg Cys Ser Met Asp Leu Lys Asn Ile Asn Phe  
95 100 105

<210> 372  
<211> 1281  
<212> DNA  
<213> Homo sapiens

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ggcaggcacc ttagtccca gctacccggg aggctgaggc aggagaatca 1200  
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<210> 373  
 <211> 229  
 <212> PRT  
 <213> Homo sapiens

<400> 373  
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 Leu Ala Asn Thr Asp Val Phe Leu Ser Lys Pro Gln Lys Ala Ala  
 35 40 45  
 Leu Glu Tyr Leu Glu Asp Ile Asp Leu Lys Thr Leu Glu Lys Glu  
 50 55 60  
 Pro Arg Thr Phe Lys Ala Lys Glu Leu Trp Glu Lys Asn Gly Ala  
 65 70 75  
 Val Ile Met Ala Val Arg Arg Pro Gly Cys Phe Leu Cys Arg Glu  
 80 85 90  
 Glu Ala Ala Asp Leu Ser Ser Leu Lys Ser Met Leu Asp Gln Leu  
 95 100 105  
 Gly Val Pro Leu Tyr Ala Val Val Lys Glu His Ile Arg Thr Glu  
 110 115 120  
 Val Lys Asp Phe Gln Pro Tyr Phe Lys Gly Glu Ile Phe Leu Asp  
 125 130 135  
 Glu Lys Lys Lys Phe Tyr Gly Pro Gln Arg Arg Lys Met Met Phe  
 140 145 150  
 Met Gly Phe Ile Arg Leu Gly Val Trp Tyr Asn Phe Phe Arg Ala  
 155 160 165  
 Trp Asn Gly Gly Phe Ser Gly Asn Leu Glu Gly Glu Gly Phe Ile  
 170 175 180  
 Leu Gly Gly Val Phe Val Val Gly Ser Gly Lys Gln Gly Ile Leu  
 185 190 195  
 Leu Glu His Arg Glu Lys Glu Phe Gly Asp Lys Val Asn Leu Leu  
 200 205 210  
 Ser Val Leu Glu Ala Ala Lys Met Ile Lys Pro Gln Thr Leu Ala  
 215 220 225  
 Ser Glu Lys Lys

<210> 374  
 <211> 744  
 <212> DNA  
 <213> Homo sapiens

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cctgccgttc ctgctggccc gctggggccg agcctggggg caaatacaga 250  
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<210> 375  
<211> 123  
<212> PRT  
<213> Homo sapiens

<400> 375  
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Thr Ser Ala Asn Glu Asn Ser Thr Val Leu Pro Ser Ser Thr Ser  
35 40 45  
Ser Ser Ser Asp Gly Asn Leu Arg Pro Glu Ala Ile Thr Ala Ile  
50 55 60  
Ile Val Val Phe Ser Leu Leu Ala Ala Leu Leu Leu Ala Val Gly  
65 70 75  
Leu Ala Leu Leu Val Arg Lys Leu Arg Glu Lys Arg Gln Thr Glu  
80 85 90  
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<212> DNA  
<213> Homo sapiens

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<210> 379

<211> 919

<212> PRT

<213> Homo sapiens

<400> 379

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Glu	Lys	Ile	Ile	Glu	Gln	Ile	Glu	Asp	Met	Val	Thr	Thr	Ala	Ser	
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Val	Ser	Ile	Leu	Ile	Pro	Glu	Asn	Trp	Lys	Glu	Asn	Pro	Gln	Tyr	
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Lys	Arg	Pro	Lys	His	Glu	Asn	His	Lys	His	Ala	Asp	Val	Ile	Val	
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Ala	Pro	Pro	Thr	Leu	Pro	Gly	Arg	Asp	Glu	Pro	Tyr	Thr	Lys	Gln	
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Phe	Thr	Glu	Cys	Gly	Glu	Lys	Gly	Glu	Tyr	Ile	His	Phe	Thr	Pro	
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Asp	Leu	Leu	Leu	Gly	Lys	Lys	Gln	Asn	Glu	Tyr	Gly	Pro	Pro	Gly	
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Lys	Leu	Phe	Val	His	Glu	Trp	Ala	His	Leu	Arg	Trp	Gly	Val	Phe	
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Asp	Glu	Tyr	Asn	Glu	Asp	Gln	Pro	Phe	Tyr	Arg	Ala	Lys	Ser	Lys	
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Lys	Ile	Glu	Ala	Thr	Arg	Cys	Ser	Ala	Gly	Ile	Ser	Gly	Arg	Asn	
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Arg	Val	Tyr	Lys	Cys	Gln	Gly	Gly	Ser	Cys	Leu	Ser	Arg	Ala	Cys	
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Arg	Ile	Asp	Ser	Thr	Thr	Lys	Leu	Tyr	Gly	Lys	Asp	Cys	Gln	Phe	
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Phe	Pro	Asp	Lys	Val	Gln	Thr	Glu	Lys	Ala	Ser	Ile	Met	Phe	Met	
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Gln	Ser	Ile	Asp	Ser	Val	Val	Glu	Phe	Cys	Asn	Glu	Lys	Thr	His	
				245					250					255	
Asn	Gln	Glu	Ala	Pro	Ser	Leu	Gln	Asn	Ile	Lys	Cys	Asn	Phe	Arg	
				260					265					270	
Ser	Thr	Trp	Glu	Val	Ile	Ser	Asn	Ser	Glu	Asp	Phe	Lys	Asn	Thr	

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	305	310	315		
Ser Met Gly Gly	Lys Asp Arg Leu Asn	Arg Met Asn Gln Ala	Ala		
	320	325	330		
Lys His Phe Leu	Leu Gln Thr Val Glu	Asn Gly Ser Trp Val	Gly		
	335	340	345		
Met Val His Phe	Asp Ser Thr Ala Thr	Ile Val Asn Lys Leu	Ile		
	350	355	360		
Gln Ile Lys Ser	Ser Asp Glu Arg Asn	Thr Leu Met Ala Gly	Leu		
	365	370	375		
Pro Thr Tyr Pro	Leu Gly Gly Thr Ser	Ile Cys Ser Gly Ile	Lys		
	380	385	390		
Tyr Ala Phe Gln	Val Ile Gly Glu Leu	His Ser Gln Leu Asp	Gly		
	395	400	405		
Ser Glu Val Leu	Leu Leu Thr Asp Gly	Glu Asp Asn Thr Ala	Ser		
	410	415	420		
Ser Cys Ile Asp	Glu Val Lys Gln Ser	Gly Ala Ile Val His	Phe		
	425	430	435		
Ile Ala Leu Gly	Arg Ala Ala Asp Glu	Ala Val Ile Glu Met	Ser		
	440	445	450		
Lys Ile Thr Gly	Gly Ser His Phe Tyr	Val Ser Asp Glu Ala	Gln		
	455	460	465		
Asn Asn Gly Leu	Ile Asp Ala Phe Gly	Ala Leu Thr Ser Gly	Asn		
	470	475	480		
Thr Asp Leu Ser	Gln Lys Ser Leu Gln	Leu Glu Ser Lys Gly	Leu		
	485	490	495		
Thr Leu Asn Ser	Asn Ala Trp Met Asn	Asp Thr Val Ile Ile	Asp		
	500	505	510		
Ser Thr Val Gly	Lys Asp Thr Phe Phe	Leu Ile Thr Trp Asn	Ser		
	515	520	525		
Leu Pro Pro Ser	Ile Ser Leu Trp Asp	Pro Ser Gly Thr Ile	Met		
	530	535	540		
Glu Asn Phe Thr	Val Asp Ala Thr Ser	Lys Met Ala Tyr Leu	Ser		
	545	550	555		
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Ala Lys Ala Asn	Pro Glu Thr Leu Thr	Ile Thr Val Thr Ser	Arg		
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Ala Ala Asn Ser	Ser Val Pro Pro Ile	Thr Val Asn Ala Lys	Met		

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Ala	Phe	Ile	Glu	Ser	Gln	Asn	Gly	His	Thr	Glu	Val	Leu	Glu	Leu
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Leu	Asp	Asn	Gly	Ala	Gly	Ala	Asp	Ser	Phe	Lys	Asn	Asp	Gly	Val
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Tyr	Ser	Arg	Tyr	Phe	Thr	Ala	Tyr	Thr	Glu	Asn	Gly	Arg	Tyr	Ser
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Leu	Lys	Val	Arg	Ala	His	Gly	Gly	Ala	Asn	Thr	Ala	Arg	Leu	Lys
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Glu	Asp	Thr	Gln	Thr	Thr	Leu	Glu	Asp	Phe	Ser	Arg	Thr	Ala	Ser
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Gly	Gly	Ala	Phe	Val	Val	Ser	Gln	Val	Pro	Ser	Leu	Pro	Leu	Pro
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Asp	Gln	Tyr	Pro	Pro	Ser	Gln	Ile	Thr	Asp	Leu	Asp	Ala	Thr	Val
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His	Glu	Asp	Lys	Ile	Ile	Leu	Thr	Trp	Thr	Ala	Pro	Gly	Asp	Asn
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Phe	Asp	Val	Gly	Lys	Val	Gln	Arg	Tyr	Ile	Ile	Arg	Ile	Ser	Ala
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Ser	Ile	Leu	Asp	Leu	Arg	Asp	Ser	Phe	Asp	Asp	Ala	Leu	Gln	Val
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Phe	Ala	Phe	Lys	Pro	Glu	Asn	Ile	Ser	Glu	Glu	Asn	Ala	Thr	His
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Lys	Val	Ser	Asn	Ile	Ala	Gln	Val	Thr	Leu	Phe	Ile	Pro	Gln	Ala
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Asn	Pro	Asp	Asp	Ile	Asp	Pro	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Pro
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Thr	Pro	Asp	Lys	Ser	His	Asn	Ser	Gly	Val	Asn	Ile	Ser	Thr	Leu
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 <212> PRT  
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 Pro Arg Ala Asn Ser Pro Thr Gly Lys Glu Gly Tyr Gln Ala Val  
 50 55 60  
 Leu Gln Glu Trp Glu Glu Gln His Arg Asn Tyr Val Ser Ser Leu  
 65 70 75  
 Lys Arg Gln Ile Ala Gln Leu Lys Glu Glu Leu Gln Glu Arg Ser  
 80 85 90

Glu	Gln	Leu	Arg	Asn	Gly	Gln	Tyr	Gln	Ala	Ser	Asp	Ala	Ala	Gly	
				95					100					105	
Leu	Gly	Leu	Asp	Arg	Ser	Pro	Pro	Glu	Lys	Thr	Gln	Ala	Asp	Leu	
				110					115					120	
Leu	Ala	Phe	Leu	His	Ser	Gln	Val	Asp	Lys	Ala	Glu	Val	Asn	Ala	
				125					130					135	
Gly	Val	Lys	Leu	Ala	Thr	Glu	Tyr	Ala	Ala	Val	Pro	Phe	Asp	Ser	
				140					145					150	
Phe	Thr	Leu	Gln	Lys	Val	Tyr	Gln	Leu	Glu	Thr	Gly	Leu	Thr	Arg	
				155					160					165	
His	Pro	Glu	Glu	Lys	Pro	Val	Arg	Lys	Asp	Lys	Arg	Asp	Glu	Leu	
				170					175					180	
Val	Glu	Ala	Ile	Glu	Ser	Ala	Leu	Glu	Thr	Leu	Asn	Asn	Pro	Ala	
				185					190					195	
Glu	Asn	Ser	Pro	Asn	His	Arg	Pro	Tyr	Thr	Ala	Ser	Asp	Phe	Ile	
				200					205					210	
Glu	Gly	Ile	Tyr	Arg	Thr	Glu	Arg	Asp	Lys	Gly	Thr	Leu	Tyr	Glu	
				215					220					225	
Leu	Thr	Phe	Lys	Gly	Asp	His	Lys	His	Glu	Phe	Lys	Arg	Leu	Ile	
				230					235					240	
Leu	Phe	Arg	Pro	Phe	Ser	Pro	Ile	Met	Lys	Val	Lys	Asn	Glu	Lys	
				245					250					255	
Leu	Asn	Met	Ala	Asn	Thr	Leu	Ile	Asn	Val	Ile	Val	Pro	Leu	Ala	
				260					265					270	
Lys	Arg	Val	Asp	Lys	Phe	Arg	Gln	Phe	Met	Gln	Asn	Phe	Arg	Glu	
				275					280					285	
Met	Cys	Ile	Glu	Gln	Asp	Gly	Arg	Val	His	Leu	Thr	Val	Val	Tyr	
				290					295					300	
Phe	Gly	Lys	Glu	Glu	Ile	Asn	Glu	Val	Lys	Gly	Ile	Leu	Glu	Asn	
				305					310					315	
Thr	Ser	Lys	Ala	Ala	Asn	Phe	Arg	Asn	Phe	Thr	Phe	Ile	Gln	Leu	
				320					325					330	
Asn	Gly	Glu	Phe	Ser	Arg	Gly	Lys	Gly	Leu	Asp	Val	Gly	Ala	Arg	
				335					340					345	
Phe	Trp	Lys	Gly	Ser	Asn	Val	Leu	Leu	Phe	Phe	Cys	Asp	Val	Asp	
				350					355					360	
Ile	Tyr	Phe	Thr	Ser	Glu	Phe	Leu	Asn	Thr	Cys	Arg	Leu	Asn	Thr	
				365					370					375	
Gln	Pro	Gly	Lys	Lys	Val	Phe	Tyr	Pro	Val	Leu	Phe	Ser	Gln	Tyr	
				380					385					390	
Asn	Pro	Gly	Ile	Ile	Tyr	Gly	His	His	Asp	Ala	Val	Pro	Pro	Leu	
				395					400					405	



Glu	Gln	Gln	Leu	Val	Ile	Lys	Lys	Glu	Thr	Gly	Phe	Trp	Arg	Asp	
				410					415					420	
Phe	Gly	Phe	Gly	Met	Thr	Cys	Gln	Tyr	Arg	Ser	Asp	Phe	Ile	Asn	
				425					430					435	
Ile	Gly	Gly	Phe	Asp	Leu	Asp	Ile	Lys	Gly	Trp	Gly	Gly	Glu	Asp	
				440					445					450	
Val	His	Leu	Tyr	Arg	Lys	Tyr	Leu	His	Ser	Asn	Leu	Ile	Val	Val	
				455					460					465	
Arg	Thr	Pro	Val	Arg	Gly	Leu	Phe	His	Leu	Trp	His	Glu	Lys	Arg	
				470					475					480	
Cys	Met	Asp	Glu	Leu	Thr	Pro	Glu	Gln	Tyr	Lys	Met	Cys	Met	Gln	
				485					490					495	
Ser	Lys	Ala	Met	Asn	Glu	Ala	Ser	His	Gly	Gln	Leu	Gly	Met	Leu	
				500					505					510	
Val	Phe	Arg	His	Glu	Ile	Glu	Ala	His	Leu	Arg	Lys	Gln	Lys	Gln	
				515					520					525	
Lys	Thr	Ser	Ser	Lys	Lys	Thr									
				530											

<210> 382  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 382  
 ctcggggaaa gggacttgat gttgg 25

<210> 383  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 383  
 gcgaaggatga gcctctatct cgtgcc 26

<210> 384  
 <211> 19  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 384  
 cagcctacac gtattgagg 19

<210> 385  
 <211> 48  
 <212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 385

cagtcagtac aatcctggca taatatacgg ccacatgat gcagtc 48

<210> 386

<211> 1346

<212> DNA

<213> Homo sapiens

<400> 386

gaaagaatgt tgtggctgct cttttttctg gtgactgcca ttcattgctga 50  
actctgtcaa ccaggtgcag aaaatgcttt taaagtgaga cttagtatca 100  
gaacagctct gggagataaa gcatatgcct gggataccaa tgaagaatac 150  
ctcttcaaag cgatggtagc tttctccatg agaaaagtgc ccaacagaga 200  
agcaacagaa atttcccatg tcctactttg caatgtaacc cagaggggtat 250  
cattctggtt tgtgggtaca gacccttcaa aaaatcacac ccttctgct 300  
gttgaggtgc aatcagccat aagaatgaac aagaaccgga tcaacaatgc 350  
cttctttcta aatgaccaa ctctggaatt tttaaaatc ccttccacac 400  
ttgcaccacc catggacca tctgtgcca tctggattat tatatttgg 450  
gtgatatttt gcatcatcat agttgcaatt gcactactga ttttatcagg 500  
gatctggcaa cgtagaagaa agaacaaga accatctgaa gtggatgacg 550  
ctgaagataa gtgtgaaaac atgatcaca ttgaaaatgg catcccctct 600  
gatcccctgg acatgaaggg gggcatatta atgatgcctt catgacagag 650  
gatgagaggc tccccctct ctgaagggt gttgttctgc ttcctcaaga 700  
aattaaacat ttgtttctgt gtgactgctg agcatcctga aataccaaga 750  
gcagatcata tttttgttt caccattctt cttttgtaat aaattttgaa 800  
tgtgcttgaa agtgaaaagc aatcaattat accaccaac accactgaaa 850  
tcataagcta ttcacgactc aaaatattct aaaatatttt tctgacagta 900  
tagtgtataa atgtggcat gtggtatttg tagttattga tttaagcatt 950  
tttagaaata agatcaggca tatgtatata ttttcacact tcaaagacct 1000  
aaggaaaaat aaattttcca gtggagaata catataatat ggtgtagaaa 1050  
tcattgaaaa tggatccttt ttgacgatca cttatatcac tctgtatatg 1100  
actaagtaaa caaagtgtg aagtaattat tgtaaatgga tggataaaaa 1150  
tggaattact catatacagg gtggaatttt atcctgttat cacaccaaca 1200  
gttgattata tttttctga atatcagccc ctaataggac aattctattt 1250

gttgaccatt tctacaattt gtaaaagtcc aatctgtgct aacttaataa 1300

agtaataatc atctcttttt aaaaaaaaaa aaaaaaaaaa aaaaaa 1346

<210> 387

<211> 212

<212> PRT

<213> Homo sapiens

<400> 387

Met Leu Trp Leu Leu Phe Phe Leu Val Thr Ala Ile His Ala Glu  
1 5 10 15

Leu Cys Gln Pro Gly Ala Glu Asn Ala Phe Lys Val Arg Leu Ser  
20 25 30

Ile Arg Thr Ala Leu Gly Asp Lys Ala Tyr Ala Trp Asp Thr Asn  
35 40 45

Glu Glu Tyr Leu Phe Lys Ala Met Val Ala Phe Ser Met Arg Lys  
50 55 60

Val Pro Asn Arg Glu Ala Thr Glu Ile Ser His Val Leu Leu Cys  
65 70 75

Asn Val Thr Gln Arg Val Ser Phe Trp Phe Val Val Thr Asp Pro  
80 85 90

Ser Lys Asn His Thr Leu Pro Ala Val Glu Val Gln Ser Ala Ile  
95 100 105

Arg Met Asn Lys Asn Arg Ile Asn Asn Ala Phe Phe Leu Asn Asp  
110 115 120

Gln Thr Leu Glu Phe Leu Lys Ile Pro Ser Thr Leu Ala Pro Pro  
125 130 135

Met Asp Pro Ser Val Pro Ile Trp Ile Ile Ile Phe Gly Val Ile  
140 145 150

Phe Cys Ile Ile Ile Val Ala Ile Ala Leu Leu Ile Leu Ser Gly  
155 160 165

Ile Trp Gln Arg Arg Arg Lys Asn Lys Glu Pro Ser Glu Val Asp  
170 175 180

Asp Ala Glu Asp Lys Cys Glu Asn Met Ile Thr Ile Glu Asn Gly  
185 190 195

Ile Pro Ser Asp Pro Leu Asp Met Lys Gly Gly Ile Leu Met Met  
200 205 210

Pro Ser

<210> 388

<211> 1371

<212> DNA

<213> Homo sapiens

<400> 388

aactcaaaact cctctctctg ggaaaacgcg gtgcttgctc ctcccggagt 50

ggcccttgga ggggtgttga gccctcggtc tgccccgtcc ggtctctggg 100  
 gccaaggctg ggtttccctc atgtatggca agagctctac tcgtgcgggtg 150  
 cttcttctcc ttggcataca gctcacagct ctttggccta tagcagctgt 200  
 ggaaatttat acctcccggg tgctggaggc tgtaaatggg acagatgctc 250  
 ggttaaaatg cactttctcc agctttgccc ctgtgggtga tgctctaaca 300  
 gtgacctgga attttcgtcc tctagacggg ggacctgagc agtttgtatt 350  
 ctactaccac atagatccct tccaacctat gagtggggcg ttaaggacc 400  
 ggggtgtcttg ggatgggaat cctgagcggg acgatgcctc catccttctc 450  
 tggaaactgc agttcgacga caatgggaca tacacctgcc aggtgaagaa 500  
 cccacctgat gttgatgggg tgatagggga gatccggctc agcgtcgtgc 550  
 acactgtacg cttctctgag atccacttcc tggtctctggc cattggctct 600  
 gcctgtgcac tgatgatcat aatagtaatt gtagtggtcc tcttccagca 650  
 ttaccgaaa aagcgatggg ccgaaagagc tcataaagtg gtggagataa 700  
 aatcaaaaga agaggaaagg ctcaaccaag agaaaaaggt ctctgtttat 750  
 ttagaagaca cagactaaca atttttagatg gaagctgaga tgatttccaa 800  
 gaacaagaac ctagtatatt cttgaagtta atggaaactt ttctttggct 850  
 tttccagttg tgacctgtt tccaaccagt tctgcagcat attagattct 900  
 agacaagcaa caccctctg gagccagcac agtgctcctc catatcacca 950  
 gtcatacaca gcctcattat taaggcttta ttttaattca gagtgtaaat 1000  
 tttttcaagt gtcattagg ttttataaac aagaagctac atttttgccc 1050  
 ttaagacact acttacagt ttatgacttg tatacacata tattggatc 1100  
 aaaggggata aaagccaatt tgtctgttac atttcctttc acgtatttct 1150  
 tttagcagca cttctgtac taaagttaat gtgtttaact tctttccttc 1200  
 ccacattctc aattaaaagg tgagctaagc ctctcgggtg tttctgatta 1250  
 acagtaaadc cttaaattcaa actgttaaat gacattttta tttttatgtc 1300  
 tctccttaac tatgagacac atcttgtttt actgaatttc tttcaatatt 1350  
 ccaggtgata gatttttgtc g 1371

<210> 389  
 <211> 215  
 <212> PRT  
 <213> Homo sapiens

<400> 389  
 Met Tyr Gly Lys Ser Ser Thr Arg Ala Val Leu Leu Leu Leu Gly  
 1 5 10 15

Ile	Gln	Leu	Thr	Ala	Leu	Trp	Pro	Ile	Ala	Ala	Val	Glu	Ile	Tyr	
				20					25					30	
Thr	Ser	Arg	Val	Leu	Glu	Ala	Val	Asn	Gly	Thr	Asp	Ala	Arg	Leu	
				35					40					45	
Lys	Cys	Thr	Phe	Ser	Ser	Phe	Ala	Pro	Val	Gly	Asp	Ala	Leu	Thr	
				50					55					60	
Val	Thr	Trp	Asn	Phe	Arg	Pro	Leu	Asp	Gly	Gly	Pro	Glu	Gln	Phe	
				65					70					75	
Val	Phe	Tyr	Tyr	His	Ile	Asp	Pro	Phe	Gln	Pro	Met	Ser	Gly	Arg	
				80					85					90	
Phe	Lys	Asp	Arg	Val	Ser	Trp	Asp	Gly	Asn	Pro	Glu	Arg	Tyr	Asp	
				95					100					105	
Ala	Ser	Ile	Leu	Leu	Trp	Lys	Leu	Gln	Phe	Asp	Asp	Asn	Gly	Thr	
				110					115					120	
Tyr	Thr	Cys	Gln	Val	Lys	Asn	Pro	Pro	Asp	Val	Asp	Gly	Val	Ile	
				125					130					135	
Gly	Glu	Ile	Arg	Leu	Ser	Val	Val	His	Thr	Val	Arg	Phe	Ser	Glu	
				140					145					150	
Ile	His	Phe	Leu	Ala	Leu	Ala	Ile	Gly	Ser	Ala	Cys	Ala	Leu	Met	
				155					160					165	
Ile	Ile	Ile	Val	Ile	Val	Val	Val	Leu	Phe	Gln	His	Tyr	Arg	Lys	
				170					175					180	
Lys	Arg	Trp	Ala	Glu	Arg	Ala	His	Lys	Val	Val	Glu	Ile	Lys	Ser	
				185					190					195	
Lys	Glu	Glu	Glu	Arg	Leu	Asn	Gln	Glu	Lys	Lys	Val	Ser	Val	Tyr	
				200					205					210	
Leu	Glu	Asp	Thr	Asp											
				215											

<210> 390  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 390  
 ccgaggccat ctagaggcca gagc 24

<210> 391  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 391  
 acaggcagag ccaatggcca gagc 24

<210> 392  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 392  
 gagaggactg cgggagtttg ggacctttgt gcagacgtgc tcatg 45

<210> 393  
 <211> 471  
 <212> DNA  
 <213> Homo sapiens

<400> 393  
 gcatttttgt ctgtgctccc tgatcttcag gtcaccacca tgaagttctt 50  
 agcagtcctg gtactcttgg gagtttccat ctttctgggc tctgcccaga 100  
 atccgacaac agctgctcca gctgacacgt atccagctac tggctctgct 150  
 gatgatgaag cccctgatgc tgaaaccact gctgctgcaa ccactgcgac 200  
 cactgctgct cctaccactg caaccaccgc tgcttctacc actgctcgta 250  
 aagacattcc agttttaccc aaatgggttg gggatctccc gaatggtaga 300  
 gtgtgtccct gagatggaat cagcttgagt cttctgcaat tggtcacaac 350  
 tattcatgct tcctgtgatt tcatccaact acttaccttg cctacgatat 400  
 cccctttatc tctaatacgt ttattttctt tcaaataaaa aataactatg 450  
 agcaacataa aaaaaaaaaa a 471

<210> 394  
 <211> 90  
 <212> PRT  
 <213> Homo sapiens

<400> 394  
 Met Lys Phe Leu Ala Val Leu Val Leu Leu Gly Val Ser Ile Phe  
 1 5 10 15  
 Leu Val Ser Ala Gln Asn Pro Thr Thr Ala Ala Pro Ala Asp Thr  
 20 25 30  
 Tyr Pro Ala Thr Gly Pro Ala Asp Asp Glu Ala Pro Asp Ala Glu  
 35 40 45  
 Thr Thr Ala Ala Ala Thr Thr Ala Thr Thr Ala Ala Pro Thr Thr  
 50 55 60  
 Ala Thr Thr Ala Ala Ser Thr Thr Ala Arg Lys Asp Ile Pro Val  
 65 70 75  
 Leu Pro Lys Trp Val Gly Asp Leu Pro Asn Gly Arg Val Cys Pro  
 80 85 90

<210> 395  
 <211> 25

<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 395  
gctccctgat cttcatgtca ccacc 25

<210> 396  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 396  
caggacaca ctctaccatt cgggag 26

<210> 397  
<211> 42  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 397  
ccatctttct ggtctctgcc cagaatcoga caacagctgc tc 42

<210> 398  
<211> 907  
<212> DNA  
<213> Homo sapiens

<400> 398  
ggactctgaa ggtcccaagc agctgctgag gcccccaagg aagtgggtcc 50  
aaccttggac ccctaggggt ctggatttgc tggttaacaa gataacctga 100  
gggcaggacc ccatagggga atgctacctc ctgcccctcc acctgccctg 150  
gtgttcacgg tggcctggtc cctccttgcc gagagagtgt cctgggtcag 200  
ggacgcagag gacgctcaca gactccagcc ctttgttacc gagaggacac 250  
ttggcaaggt ccagcgatgg tccggagtcc acacacagac tggcggcagg 300  
gcaggagggg gacagttctg ttgtgcttgg ttggacagta agaggggtctt 350  
ggccagtcca gggtaggggg cggcaaactc cataaagaac cagaggggtct 400  
gggccccggc cacagagtca totgcccagc tcctctgctg ctggccagtg 450  
ggagtggcac gaggtggggc tttgtgccag taaaaccaca ggctggattt 500  
gcctgcgggc catggtccct gtctagggca gcaattctca accttcttgc 550  
tctcaggacc ccaaagagct ttcatgtat ctattgattt ttaccacatt 600  
agcaattaa actgagaaat gggccgggca cggtaggctca cgctgtaat 650

cccagcactt tgggaggccg aggcgggtgg atcacctgag atcaggagtt 700  
 caagaccagc ctggccaaca tggtgaaacc ttgtctacta aaaatacaaa 750  
 aaattagcca ggcacagtgg tgtgcactgg tagtcccagt tactcgggag 800  
 gctgaggcag gaaaatcgct tgaacccagg aggcggacgt tgcggtgagc 850  
 cgagatcgcg ccgctgattc cagcctgggc gacaagagtg agactccatc 900  
 tcacaca 907

<210> 399  
 <211> 120  
 <212> PRT  
 <213> Homo sapiens

<400> 399  
 Met Leu Pro Pro Ala Leu Pro Pro Ala Leu Val Phe Thr Val Ala  
 1 5 10 15  
 Trp Ser Leu Leu Ala Glu Arg Val Ser Trp Val Arg Asp Ala Glu  
 20 25 30  
 Asp Ala His Arg Leu Gln Pro Phe Val Thr Glu Arg Thr Leu Gly  
 35 40 45  
 Lys Val Gln Arg Trp Ser Gly Val His Thr Gln Thr Gly Gly Arg  
 50 55 60  
 Ala Gly Gly Gly Gln Phe Cys Cys Ala Trp Leu Asp Ser Lys Arg  
 65 70 75  
 Val Leu Ala Ser Pro Gly Trp Gly Ala Ala Asn Ser Ile Lys Asn  
 80 85 90  
 Gln Arg Val Trp Ala Pro Ala Thr Glu Ser Ser Ala Gln Leu Leu  
 95 100 105  
 Cys Cys Trp Pro Val Gly Val Ala Arg Gly Gly Ala Leu Cys Gln  
 110 115 120

<210> 400  
 <211> 893  
 <212> DNA  
 <213> Homo sapiens

<400> 400  
 gtcatgccag tgccgtctct gtgcctgctc tgggccctgg caatggtgac 50  
 ccggcctgcc tcagcggccc ccatgggagg cccagaactg gcacagcatg 100  
 aggagctgac cctgctcttc catgggaccc tgcagctggg ccaggccctc 150  
 aacggtgtgt acaggaccac ggaggggacgg ctgacaaagg ccaggaacag 200  
 cctgggtctc tatggccgca caatagaact cctggggcag gaggtcagcc 250  
 ggggccggga tgcagcccag gaacttcggg caagcctgtt ggagactcag 300  
 atggaggagg atattctgca gctgcaggca gaggccacag ctgaggtgct 350  
 gggggagggtg gcccaggcac agaaggtgct acgggacagc gtgcagcggc 400



tagaagtcca gctgaggagc gcctggctgg gccctgccta ccgagaattt 450  
 gaggtcttaa aggetcacgc tgacaagcag agccacatcc tatgggccct 500  
 cacaggccac gtgcagcggc agaggcggga gatggtggca cagcagcatc 550  
 ggctgcgaca gatccaggag agactccaca cagcggcgct cccagcctga 600  
 atctgcctgg atggaactga ggaccaatca tgctgcaagg aacacttcca 650  
 cgccccgtga ggccccctgtg cagggaggag ctgcctgttc actgggatca 700  
 gccagggcgc cgggccccac ttctgagcac agagcagaga cagacgcagg 750  
 cggggacaaa ggcagaggat gtagcccat tggggagggg tggaggaagg 800  
 acatgtaccc tttcatgcct acacaccct cattaagca gagtcgtggc 850  
 atttcaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 893

<210> 401  
 <211> 198  
 <212> PRT  
 <213> Homo sapiens

<400> 401  
 Met Pro Val Pro Ala Leu Cys Leu Leu Trp Ala Leu Ala Met Val  
 1 5 10 15  
 Thr Arg Pro Ala Ser Ala Ala Pro Met Gly Gly Pro Glu Leu Ala  
 20 25 30  
 Gln His Glu Glu Leu Thr Leu Leu Phe His Gly Thr Leu Gln Leu  
 35 40 45  
 Gly Gln Ala Leu Asn Gly Val Tyr Arg Thr Thr Glu Gly Arg Leu  
 50 55 60  
 Thr Lys Ala Arg Asn Ser Leu Gly Leu Tyr Gly Arg Thr Ile Glu  
 65 70 75  
 Leu Leu Gly Gln Glu Val Ser Arg Gly Arg Asp Ala Ala Gln Glu  
 80 85 90  
 Leu Arg Ala Ser Leu Leu Glu Thr Gln Met Glu Glu Asp Ile Leu  
 95 100 105  
 Gln Leu Gln Ala Glu Ala Thr Ala Glu Val Leu Gly Glu Val Ala  
 110 115 120  
 Gln Ala Gln Lys Val Leu Arg Asp Ser Val Gln Arg Leu Glu Val  
 125 130 135  
 Gln Leu Arg Ser Ala Trp Leu Gly Pro Ala Tyr Arg Glu Phe Glu  
 140 145 150  
 Val Leu Lys Ala His Ala Asp Lys Gln Ser His Ile Leu Trp Ala  
 155 160 165  
 Leu Thr Gly His Val Gln Arg Gln Arg Arg Glu Met Val Ala Gln  
 170 175 180  
 Gln His Arg Leu Arg Gln Ile Gln Glu Arg Leu His Thr Ala Ala

Leu Pro Ala

<210> 402  
 <211> 1915  
 <212> DNA  
 <213> Homo sapiens

<400> 402  
 ggcaacatgg ctcagcaggc ttgccccaga gccatggcaa agaattggact 50  
 tgtaattttgc atcctggtga tcaccttact cctggaccag accaccagcc 100  
 acacatccag attaaaagcc aggaagcaca gcaaacgtcg agtgagagac 150  
 aaggatggag atctgaagac tcaaattgaa aagctctgga cagaagtcaa 200  
 tgccttgaag gaaattcaag ccctgcagac agtctgtctc cgaggcacta 250  
 aagttcaciaa gaaatgctac cttgcttcag aaggtttgaa gcatttccat 300  
 gaggccaatg aagactgcat ttccaaagga ggaatcctgg ttatccccag 350  
 gaactccgac gaaatcaacg ccctccaaga ctatggtaaa aggagcctgc 400  
 cagggtgtcaa tgacttttgg ctgggcatca atgacatggt cacggaaggc 450  
 aagtttgttg acgtcaacgg aatcgctatc tccttcctca actgggaccg 500  
 tgcacagcct aacggtggca agcgagaaaa ctgtgtcctg ttctcccaat 550  
 cagctcaggg caagtggagt gatgaggcct gtcgcagcag caagagatac 600  
 atatgcgagt tcaccatccc taaataggto tttctccaat gtgtcctcca 650  
 agcaagattc atcataactt ataggttcat gatctctaag atcaagtaaa 700  
 aatcataatt tttacttatt aaaaaattgc aacacaagat caatgtccat 750  
 agcaatatga tagcatcagc caattttgct aacacatttc tttgggattt 800  
 tgcccttcct ggggtatagg ggatcagaaa tattgatcca tgtgcacgca 850  
 gataaaaatgg cttctgctaa acagactaaa atctttctct ctagtctttc 900  
 tcacttgtag aaaccagtt tgttttcaaa aaatcacagt agcaatgcaa 950  
 ctcatcactc tagaaaagca agcttaggct acctgaaaga tttcccttg 1000  
 gaagtttagc gtatgtttga ctaacaaaaa ttccctacat cagagactct 1050  
 aggtgctata taatccaaaa acttttcagc ctgttgctca ttctgtccca 1100  
 tgctggcaat aataccttgt cagccatta cccttatttt gaattgctcc 1150  
 atctcctggt gggacttgta tcttgtctgc catatcagaa cacaaacccc 1200  
 tgaagaggtt ctgatttgat tttttttttt tcttcatgcc tacccttttt 1250  
 ttggaagttt ccagccgcaa tttgaaatga aatgacaagg tgtatatttg 1300

atcaattttc attcccacca ttgcattaca acctctaact taaatgggta 1350  
 accctaaggc atatcaaaga agcagattgc atgataaacg gaaatagaaa 1400  
 aaaagaacct acattttattt tgcttttagca tccttactct caccttttat 1450  
 gagattgaga gtggacttac atttcctttt ttacattttc gtatatttat 1500  
 ttttttttagc catcattata tgtttaagtc tattatgggc aaccaatctt 1550  
 tggaagctga aaactgaatt taaagaatgc tatcttggaa aattgcatac 1600  
 gtctgtgcaa ttttttattc tgcctagtgc tattctgctt gtttaactag 1650  
 attgtacaaa ataacttcat tgcttaatat caaattacaa agtttagact 1700  
 tggagggaaa tgggcttttt agaagcaaac aattttaaat atattttgtt 1750  
 cttcaaataa atagtgttta aacattgaat gtgttttgtg aacaatatcc 1800  
 cactttgcaa actttaacta cacatgcttg gaattaagtt ttagctgttt 1850  
 tcattgctca ataataaagc ctgaattctg atcaataaaa aaaaaaaaaa 1900  
 aaaaaaaaaa aaaaa 1915

<210> 403  
 <211> 206  
 <212> PRT  
 <213> Homo sapiens

<400> 403  
 Met Ala Gln Gln Ala Cys Pro Arg Ala Met Ala Lys Asn Gly Leu  
 1 5 10 15  
 Val Ile Cys Ile Leu Val Ile Thr Leu Leu Leu Asp Gln Thr Thr  
 20 25 30  
 Ser His Thr Ser Arg Leu Lys Ala Arg Lys His Ser Lys Arg Arg  
 35 40 45  
 Val Arg Asp Lys Asp Gly Asp Leu Lys Thr Gln Ile Glu Lys Leu  
 50 55 60  
 Trp Thr Glu Val Asn Ala Leu Lys Glu Ile Gln Ala Leu Gln Thr  
 65 70 75  
 Val Cys Leu Arg Gly Thr Lys Val His Lys Lys Cys Tyr Leu Ala  
 80 85 90  
 Ser Glu Gly Leu Lys His Phe His Glu Ala Asn Glu Asp Cys Ile  
 95 100 105  
 Ser Lys Gly Gly Ile Leu Val Ile Pro Arg Asn Ser Asp Glu Ile  
 110 115 120  
 Asn Ala Leu Gln Asp Tyr Gly Lys Arg Ser Leu Pro Gly Val Asn  
 125 130 135  
 Asp Phe Trp Leu Gly Ile Asn Asp Met Val Thr Glu Gly Lys Phe  
 140 145 150  
 Val Asp Val Asn Gly Ile Ala Ile Ser Phe Leu Asn Trp Asp Arg

	155		160		165
Ala Gln Pro Asn Gly Gly Lys Arg Glu Asn Cys Val Leu Phe Ser	170		175		180
Gln Ser Ala Gln Gly Lys Trp Ser Asp Glu Ala Cys Arg Ser Ser	185		190		195
Lys Arg Tyr Ile Cys Glu Phe Thr Ile Pro Lys	200		205		

<210> 404  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 404  
 cctggttatc cccaggaact ccgac 25

<210> 405  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 405  
 ctcttgctgc tgcgacaggc ctc 23

<210> 406  
 <211> 46  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 406  
 cgccctccaa gactatggta aaaggagcct gccagggtgc aatgac 46

<210> 407  
 <211> 570  
 <212> DNA  
 <213> Homo sapiens

<400> 407  
 gcgaggaccg ggtataagaa gcctcgtggc ottgcccggg cagccgcagg 50  
 ttccccgcgc gccccgagcc cccgcgccat gaagctcgcc gccctcctgg 100  
 ggctctgcgt ggccctgtcc tgcagctccg ctgctgcttt cttagtgggc 150  
 tcggccaagc ctgtggccca gcctgtcgct gcgctggagt cggcggcgga 200  
 ggccggggcc gggaccctgg ccaacccccct cggcaccctc aaccgctga 250  
 agctcctgct gaggagcctg ggcatccccg tgaaccacct catagagggc 300  
 tcccagaagt gtgtggctga gctgggtccc caggccgtgg gggccgtgaa 350

ggccctgaag gccctgctgg gggccctgac agtgtttggc tgagccgaga 400  
ctggagcatc tacacctgag gacaagacgc tgcccacccg cgagggctga 450  
aaaccccgcc gcggggagga ccgtccatcc ccttcccccg gccctctca 500  
ataaacgtgg ttaagagcaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 550  
aaaaaaaaaa aaaaaaaaaa 570

<210> 408  
<211> 104  
<212> PRT  
<213> Homo sapiens

<400> 408  
Met Lys Leu Ala Ala Leu Leu Gly Leu Cys Val Ala Leu Ser Cys  
1 5 10 15  
Ser Ser Ala Ala Ala Phe Leu Val Gly Ser Ala Lys Pro Val Ala  
20 25 30  
Gln Pro Val Ala Ala Leu Glu Ser Ala Ala Glu Ala Gly Ala Gly  
35 40 45  
Thr Leu Ala Asn Pro Leu Gly Thr Leu Asn Pro Leu Lys Leu Leu  
50 55 60  
Leu Ser Ser Leu Gly Ile Pro Val Asn His Leu Ile Glu Gly Ser  
65 70 75  
Gln Lys Cys Val Ala Glu Leu Gly Pro Gln Ala Val Gly Ala Val  
80 85 90  
Lys Ala Leu Lys Ala Leu Leu Gly Ala Leu Thr Val Phe Gly  
95 100

<210> 409  
<211> 2089  
<212> DNA  
<213> Homo sapiens

<400> 409  
tgaaggactt ttccaggacc caaggccaca cactggaagt cttgcagctg 50  
aaggaggca ctcttggcc tcgcagccg atcacatgaa ggtggtgcc 100  
agtctctgc tctcgtcct cctggcacag gtgtggctgg taccggctt 150  
ggccccagt cctcagtcgc cagagacccc agcccctcag aaccagacca 200  
gcagggtagt gcaggctccc agggaggaag aggaagatga gcaggaggcc 250  
agcgaggaga aggccggtga ggaagagaaa gcctggctga tggccagcag 300  
gcagcagctt gccaaaggaga cttcaaactt cggattcagc ctgctgcgaa 350  
agatctccat gaggcacgat ggcaacatgg tcttctctcc atttggcatg 400  
tccttggcca tgacaggctt gatgctgggg gccacagggc cgactgaaac 450  
ccagatcaag agagggtcc acttgaggc cctgaagccc accaagccg 500

ggctcctgcc ttccctcttt aagggaactca gagagaccct ctcccgaac 550  
 ctggaactgg gcctctcaca ggggagtttt gccttcatcc acaaggattt 600  
 tgatgtcaaa gagactttct tcaattttatc caagagggtat tttgatacag 650  
 agtgcgtgcc tatgaatttt cgcaatgcct cacaggccaa aaggctcatg 700  
 aatcattaca ttaacaaaga gactcggggg aaaattccca aactgtttga 750  
 tgagattaat cctgaaacca aattaattct tgtggattac atcttgttca 800  
 aagggaatg gttgacccca tttgaccctg tcttcaccga agtcgacact 850  
 ttccacctgg acaagtacaa gaccattaag gtgcccata tgtacgggtgc 900  
 aggcaagttt gcctccacct ttgacaagaa ttttcgttgt catgtcctca 950  
 aactgcccta ccaaggaaat gccaccatgc tgggtggtcct catggagaaa 1000  
 atgggtgacc acctcgccct tgaagactac ctgaccacag acttggtgga 1050  
 gacatggctc agaaacatga aaaccagaaa catggaagtt ttctttccga 1100  
 agttcaagct agatcagaag tatgagatgc atgagctgct taggcagatg 1150  
 ggaatcagaa gaatcttctc accttttgct gaccttagtg aactctcagc 1200  
 tactggaaga aatctccaag tatccagggt tttacgaaga acagtgattg 1250  
 aagttgatga aaggggcaact gaggcagtgg caggaatctt gtcagaaatt 1300  
 actgcttatt ccatgcctcc tgatcatcaa gtggaccggc catttcattt 1350  
 catgatctat gaagaaacct ctggaatgct tctgtttctg ggcagggtgg 1400  
 tgaatccgac tctcctataa ttcaggacat gcataagcac ttcgtgctgt 1450  
 agtagatgct gaatctgagg tatcaaacac acacaggata ccagcaatgg 1500  
 atggcagggg agagtgttcc ttttgttctt aactagttaa ggggtgttctc 1550  
 aaataaatac agtagtcccc acttatctga gggggataca ttcaaagacc 1600  
 cccagcagat gcctgaaacg gtggacagtg ctgaacctta tatatatttt 1650  
 ttcctacaca tacataccta tgataaagtt taatttataa attaggcaca 1700  
 gtaagagatt aacaataata acaacattaa gtaaaatgag ttacttgaac 1750  
 gcaagcactg caataccata acagtcaaac tgattataga gaaggctact 1800  
 aagtgactca tgggcgagga gcatagacag tgtggagaca ttgggcaagg 1850  
 ggagaattca catcctgggt gggacagagc aggacgatgc aagattccat 1900  
 cccactactc agaatggcat gctgcttaag acttttagat tgtttatattc 1950  
 tggaattttt catttaatgt ttttgacca tggttgacca tggttaactg 2000  
 agactgcaga aagcaaaacc atggataagg gaggactact acaaaagcat 2050  
 taaattgata catatttttt aaaaaaaaaa aaaaaaaaaa 2089

[illegible]

355

His Val Leu Lys	Leu Pro Tyr Gln Gly	Asn Ala Thr Met Leu Val	290	295	300
Val Leu Met Glu	Lys Met Gly Asp His	Leu Ala Leu Glu Asp Tyr	305	310	315
Leu Thr Thr Asp	Leu Val Glu Thr Trp	Leu Arg Asn Met Lys Thr	320	325	330
Arg Asn Met Glu	Val Phe Phe Pro Lys	Phe Lys Leu Asp Gln Lys	335	340	345
Tyr Glu Met His	Glu Leu Leu Arg Gln	Met Gly Ile Arg Arg Ile	350	355	360
Phe Ser Pro Phe	Ala Asp Leu Ser Glu	Leu Ser Ala Thr Gly Arg	365	370	375
Asn Leu Gln Val	Ser Arg Val Leu Arg	Arg Thr Val Ile Glu Val	380	385	390
Asp Glu Arg Gly	Thr Glu Ala Val Ala	Gly Ile Leu Ser Glu Ile	395	400	405
Thr Ala Tyr Ser	Met Pro Pro Val Ile	Lys Val Asp Arg Pro Phe	410	415	420
His Phe Met Ile	Tyr Glu Glu Thr Ser	Gly Met Leu Leu Phe Leu	425	430	435
Gly Arg Val Val	Asn Pro Thr Leu Leu		440		

<210> 411  
 <211> 636  
 <212> DNA  
 <213> Homo sapiens

<400> 411  
 ctgggatcag ccactgcagc tccctgagca ctctctacag agacgcggac 50  
 cccagacatg aggaggctcc tcctgggtcac cagcctggtg gttgtgctgc 100  
 tgtgggaggc aggtgcagtc ccagcaccca aggtccctat caagatgcaa 150  
 gtcaaacact ggccctcaga gcaggaccca gagaaggcct ggggcgcccc 200  
 tgtggtggag cctccggaga aggacgacca gctggtggtg ctgttccctg 250  
 tccagaagcc gaaactcttg accaccgagg agaagccacg aggtcagggc 300  
 aggggccccca tccttccagg caccaaggcc tggatggaga ccgaggacac 350  
 cctggggccgt gtcctgagtc ccgagcccga ccatgacagc ctgtaccacc 400  
 ctccgcctga ggaggaccag ggcgaggaga ggccccggtt gtgggtgatg 450  
 ccaaatacacc aggtgctcct gggaccggag gaagaccaag accacatcta 500  
 ccacccccag tagggctcca ggggccatca ctgccccgc cctgtcccaa 550  
 ggcccaggct gttgggactg ggaccctccc taccctgccc cagctagaca 600



aataaacccc agcaggcaaa aaaaaaaaaa aaaaaa 636

<210> 412

<211> 151

<212> PRT

<213> Homo sapiens

<400> 412

Met Arg Arg Leu Leu Leu Val Thr Ser Leu Val Val Val Leu Leu  
1 5 10 15

Trp Glu Ala Gly Ala Val Pro Ala Pro Lys Val Pro Ile Lys Met  
20 25 30

Gln Val Lys His Trp Pro Ser Glu Gln Asp Pro Glu Lys Ala Trp  
35 40 45

Gly Ala Arg Val Val Glu Pro Pro Glu Lys Asp Asp Gln Leu Val  
50 55 60

Val Leu Phe Pro Val Gln Lys Pro Lys Leu Leu Thr Thr Glu Glu  
65 70 75

Lys Pro Arg Gly Gln Gly Arg Gly Pro Ile Leu Pro Gly Thr Lys  
80 85 90

Ala Trp Met Glu Thr Glu Asp Thr Leu Gly Arg Val Leu Ser Pro  
95 100 105

Glu Pro Asp His Asp Ser Leu Tyr His Pro Pro Pro Glu Glu Asp  
110 115 120

Gln Gly Glu Glu Arg Pro Arg Leu Trp Val Met Pro Asn His Gln  
125 130 135

Val Leu Leu Gly Pro Glu Glu Asp Gln Asp His Ile Tyr His Pro  
140 145 150

Gln

<210> 413

<211> 1176

<212> DNA

<213> Homo sapiens

<400> 413

agaaagctgc actctgttga gctccagggc gcagtggagg gagggagtga 50

aggagctctc tgtacccaag gaaagtgcag ctgagactca gacaagatta 100

caatgaacca actcagcttc ctgctgtttc tcatagcgac caccagagga 150

tggagtacag atgaggctaa tacttacttc aaggaatgga cctgttcttc 200

gtctccatct ctgcccagaa gctgcaagga aatcaaagac gaatgtccta 250

gtgcatttga tggcctgtat tttctccgca ctgagaatgg tggtatctac 300

cagaccttct gtgacatgac ctctgggggt ggcggtgga cctggtggc 350

cagcgtgcat gagaatgaca tgcgtgggaa gtgcacggtg ggcatcgct 400

ggtccagtca gcagggcagc aaagcagact acccagaggg ggacggcaac 450  
 tgggccaaact acaacacctt tggatctgca gaggcggcca cgagcgatga 500  
 ctacaagaac cctgggtact acgacatoca ggccaaggac ctgggcatct 550  
 ggcacgtgcc caataagtcc cccatgcagc actggagaaa cagctccctg 600  
 ctgaggtacc gcacggacac tggcttcctc cagacactgg gacataatct 650  
 gtttggcatc taccagaaat atccagtga atattggagaa ggaaagtgtt 700  
 ggactgacaa cggcccgtg atccctgtgg tctatgattt tggcgacgcc 750  
 cagaaaacag catcttatta ctcacctat ggccagcggg aattcactgc 800  
 gggatttgtt cagttcaggg tatttaataa cgagagagca gccaacgcct 850  
 tgtgtgctgg aatgagggc accgatgta aactgagca tctactgcatt 900  
 ggtggaggag gatactttcc agaggccagt cccagcagt gtggagattt 950  
 ttctggtttt gattggagtg gatatggaac tcatgttggg tacagcagca 1000  
 gccgtgagat aactgaggca gctgtgcttc tattctatcg ttgagagttt 1050  
 tgtgggaggg aaccagacc tctcctccca accatgagat cccaaggatg 1100  
 gagaacaact taccagtag ctagaatgtt aatggcagaa gagaaaacaa 1150  
 taaatcatat tgactcaaga aaaaaa 1176

<210> 414

<211> 313

<212> PRT

<213> Homo sapiens

<400> 414

Met	Asn	Gln	Leu	Ser	Phe	Leu	Leu	Phe	Leu	Ile	Ala	Thr	Thr	Arg
1				5					10					15
Gly	Trp	Ser	Thr	Asp	Glu	Ala	Asn	Thr	Tyr	Phe	Lys	Glu	Trp	Thr
				20					25					30
Cys	Ser	Ser	Ser	Pro	Ser	Leu	Pro	Arg	Ser	Cys	Lys	Glu	Ile	Lys
				35					40					45
Asp	Glu	Cys	Pro	Ser	Ala	Phe	Asp	Gly	Leu	Tyr	Phe	Leu	Arg	Thr
				50					55					60
Glu	Asn	Gly	Val	Ile	Tyr	Gln	Thr	Phe	Cys	Asp	Met	Thr	Ser	Gly
				65					70					75
Gly	Gly	Gly	Trp	Thr	Leu	Val	Ala	Ser	Val	His	Glu	Asn	Asp	Met
				80					85					90
Arg	Gly	Lys	Cys	Thr	Val	Gly	Asp	Arg	Trp	Ser	Ser	Gln	Gln	Gly
				95					100					105
Ser	Lys	Ala	Asp	Tyr	Pro	Glu	Gly	Asp	Gly	Asn	Trp	Ala	Asn	Tyr
				110					115					120
Asn	Thr	Phe	Gly	Ser	Ala	Glu	Ala	Ala	Thr	Ser	Asp	Asp	Tyr	Lys

125	130	135
Asn Pro Gly Tyr Tyr Asp Ile Gln Ala	Lys Asp Leu Gly Ile Trp	
140	145	150
His Val Pro Asn Lys Ser Pro Met Gln	His Trp Arg Asn Ser Ser	
155	160	165
Leu Leu Arg Tyr Arg Thr Asp Thr Gly	Phe Leu Gln Thr Leu Gly	
170	175	180
His Asn Leu Phe Gly Ile Tyr Gln Lys	Tyr Pro Val Lys Tyr Gly	
185	190	195
Glu Gly Lys Cys Trp Thr Asp Asn Gly	Pro Val Ile Pro Val Val	
200	205	210
Tyr Asp Phe Gly Asp Ala Gln Lys Thr	Ala Ser Tyr Tyr Ser Pro	
215	220	225
Tyr Gly Gln Arg Glu Phe Thr Ala Gly	Phe Val Gln Phe Arg Val	
230	235	240
Phe Asn Asn Glu Arg Ala Ala Asn Ala	Leu Cys Ala Gly Met Arg	
245	250	255
Val Thr Gly Cys Asn Thr Glu His His	Cys Ile Gly Gly Gly Gly	
260	265	270
Tyr Phe Pro Glu Ala Ser Pro Gln Gln	Cys Gly Asp Phe Ser Gly	
275	280	285
Phe Asp Trp Ser Gly Tyr Gly Thr His	Val Gly Tyr Ser Ser Ser	
290	295	300
Arg Glu Ile Thr Glu Ala Ala Val Leu	Leu Phe Tyr Arg	
305	310	

<210> 415  
 <211> 1281  
 <212> DNA  
 <213> Homo sapiens

<400> 415  
 gcggagccgg cgccggctgc gcagaggagc cgctctcgcc gccgccacct 50  
 cggtggggag cccacgaggc tgccgcatcc tgccctcgga acaatgggac 100  
 tcggcgcgcg aggtgcttgg gccgcgctgc tcctggggac gctgcaggtg 150  
 ctacgcgtgc tgggggcccgc ccatgaaagc gcagccatgg cggcatctgc 200  
 aaacatagag aattctgggc ttccacacaa ctccagtgtc aactcaacag 250  
 agactctcca acatgtgcct totgaccata caaatgaaac ttccaacagt 300  
 actgtgaaac caccaacttc agttgcctca gactccagta atacaacggt 350  
 caccacatg aaacctacag cggcattctaa tacaacaaca ccagggatgg 400  
 totcaacaaa tatgacttct accacottaa agtctacacc caaaacaaca 450  
 agtgtttcac agaacacatc tcagatatca acatccacaa tgaccgtaac 500

ccacaatagt tcagtgcacat ctgctgcttc atcagtaaca atcacaacaa 550  
ctatgcattc tgaagcaaag aaaggatcaa aatttgatac tgggagcttt 600  
gttgggtgga ttgtattaac gctgggaggt ttatctattc tttacattgg 650  
atgcaaaatg tattactcaa gaagaggcat tcggtatcga accatagatg 700  
aacatgatgc catcatttaa ggaaatccat ggaccaagga tggaatacag 750  
attgatgctg ccctatcaat taatttttgt ttattaatag tttaaaacaa 800  
tattctcttt ttgaaaatag tataaacagg ccatgcatat aatgtacagt 850  
gtattacgta aatatgtaaa gattcttcaa ggtaacaagg gtttgggttt 900  
tgaaataaac atctggatct tatagaccgt tcatacaatg gttttagcaa 950  
gttcatagta agacaaacaa gtcctatctt ttttttttgg ctggggtggg 1000  
ggcattggtc acatatgacc agtaattgaa agacgtcatc actgaaagac 1050  
agaatgccat ctgggcatac aaataagaag tttgtcacag cactcaggat 1100  
tttgggtatc ttttgtagct cacataaaga acttcagtgc ttttcagagc 1150  
tgatataatc ttaattacta atgccacaca gaaattatac aatcaaacta 1200  
gatctgaagc ataatttaag aaaaacatca acattttttg tgctttaaac 1250  
tgtagtagtt ggtctagaaa caaaatactc c 1281

<210> 416  
<211> 208  
<212> PRT  
<213> Homo sapiens

<400> 416  
Met Gly Leu Gly Ala Arg Gly Ala Trp Ala Ala Leu Leu Leu Gly  
1 5 10 15  
Thr Leu Gln Val Leu Ala Leu Leu Gly Ala Ala His Glu Ser Ala  
20 25 30  
Ala Met Ala Ala Ser Ala Asn Ile Glu Asn Ser Gly Leu Pro His  
35 40 45  
Asn Ser Ser Ala Asn Ser Thr Glu Thr Leu Gln His Val Pro Ser  
50 55 60  
Asp His Thr Asn Glu Thr Ser Asn Ser Thr Val Lys Pro Pro Thr  
65 70 75  
Ser Val Ala Ser Asp Ser Ser Asn Thr Thr Val Thr Thr Met Lys  
80 85 90  
Pro Thr Ala Ala Ser Asn Thr Thr Thr Pro Gly Met Val Ser Thr  
95 100 105  
Asn Met Thr Ser Thr Thr Leu Lys Ser Thr Pro Lys Thr Thr Ser  
110 115 120  
Val Ser Gln Asn Thr Ser Gln Ile Ser Thr Ser Thr Met Thr Val

	125		130		135
Thr His Asn Ser	Ser Val Thr Ser Ala	Ala Ser Ser Val Thr	Ile		
	140	145	150		
Thr Thr Thr Met	His Ser Glu Ala Lys	Lys Gly Ser Lys Phe	Asp		
	155	160	165		
Thr Gly Ser Phe	Val Gly Gly Ile Val	Leu Thr Leu Gly Val	Leu		
	170	175	180		
Ser Ile Leu Tyr	Ile Gly Cys Lys Met	Tyr Tyr Ser Arg Arg	Gly		
	185	190	195		
Ile Arg Tyr Arg	Thr Ile Asp Glu His	Asp Ala Ile Ile			
	200	205			

<210> 417  
 <211> 1728  
 <212> DNA  
 <213> Homo sapiens

<400> 417  
 cagccgggtc ccaagcctgt gcctgagcct gagcctgagc ctgagcccga 50  
 gccgggagcc ggtcgcgggg gctcggggct gtgggaccgc tgggccccca 100  
 gcgatggcga ccctgtgggg aggccttctt cggcttggct ccttgctcag 150  
 cctgtcgtgc ctggcgcttt ccgtgctgct gctggcgag ctgtcagacg 200  
 ccgccaagaa ttctgaggat gtcagatgta aatgtatctg ccctccctat 250  
 aaagaaaatt ctgggcataa ttataataag aacatatctc agaaagattg 300  
 tgattgcctt catgttgttg agcccatgcc tgtgcggggg cctgatgtag 350  
 aagcatactg tctacgctgt gaatgcaaat atgaagaaag aagctctgtc 400  
 acaatcaagg ttaccattat aatttatctc tccatttttg gccttctaact 450  
 tctgtacatg gtatatctta ctctggttga gccatactg aagaggcgcc 500  
 tctttggaca tgcacagttg atacagagtg atgatgatat tggggatcac 550  
 cagccttttg caaatgcaca cgatgtgcta gcccgctccc gcagtcgagc 600  
 caacgtgctg aacaaggtag aatatgcaca gcagcgctgg aagcttcaag 650  
 tccaagagca gcgaaagtct gtctttgacc ggcatgttgt cctcagctaa 700  
 ttgggaattg aattcaaggt gactagaaag aaacaggcag acaactggaa 750  
 agaactgact gggttttgct gggtttcatt ttaatacctt gttgatttca 800  
 ccaactgttg ctggaagatt caaaaactgga agcaaaaact tgcttgattt 850  
 ttttttcttg ttaacgtaat aatagagaca tttttaaaag cacacagctc 900  
 aaagtcagcc aataagtctt ttcctatttg tgacttttac taataaaaat 950  
 aaatctgcct gtaaattatc ttgaagtcct ttacctggaa caagcactct 1000

ctttttcacc acatagtttt aacttgactt tcaagataat tttcaggggtt 1050  
 tttgttggtt ttgttttttg tttgtttggt ttggtgggag aggggagggg 1100  
 tgcctgggaa gtggttaaca acttttttca agtcacttta ctaaacaaac 1150  
 ttttgtaaag agacottacc ttctattttc gagtttcatt tatattttgc 1200  
 agtgtagcca gcctcatcaa agagctgact tactcatttg acttttgcac 1250  
 tgactgtatt atctgggtat ctgctgtgtc tgcacttcat ggtaaacggg 1300  
 atctaaaatg cctgggtggct tttcacaaaa agcagatttt cttcatgtac 1350  
 tgtgatgtct gatgcaatgc atcctagaac aaactggcca tttgctagtt 1400  
 tactctaaag actaaacata gtcttgggtg gtgtgggtctt actcatcttc 1450  
 tagtaccttt aaggacaaaat cctaaggact tggacacttg caataaagaa 1500  
 attttatttt aaacccaagc ctccctggat tgataatata tacacatttg 1550  
 tcagcatttc cggtcgtggt gagaggcagc tgtttgagct ccaatatgtg 1600  
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 Ser Asp Ala Ala Lys Asn Phe Glu Asp Val Arg Cys Lys Cys Ile  
 35 40 45  
 Cys Pro Pro Tyr Lys Glu Asn Ser Gly His Ile Tyr Asn Lys Asn  
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 Ile Ser Gln Lys Asp Cys Asp Cys Leu His Val Val Glu Pro Met  
 65 70 75  
 Pro Val Arg Gly Pro Asp Val Glu Ala Tyr Cys Leu Arg Cys Glu  
 80 85 90  
 Cys Lys Tyr Glu Glu Arg Ser Ser Val Thr Ile Lys Val Thr Ile  
 95 100 105  
 Ile Ile Tyr Leu Ser Ile Leu Gly Leu Leu Leu Tyr Met Val  
 110 115 120  
 Tyr Leu Thr Leu Val Glu Pro Ile Leu Lys Arg Arg Leu Phe Gly  
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His	Ala	Gln	Leu	Ile	Gln	Ser	Asp	Asp	Asp	Ile	Gly	Asp	His	Gln
				140					145					150
Pro	Phe	Ala	Asn	Ala	His	Asp	Val	Leu	Ala	Arg	Ser	Arg	Ser	Arg
				155					160					165
Ala	Asn	Val	Leu	Asn	Lys	Val	Glu	Tyr	Ala	Gln	Gln	Arg	Trp	Lys
				170					175					180
Leu	Gln	Val	Gln	Glu	Gln	Arg	Lys	Ser	Val	Phe	Asp	Arg	His	Val
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Val Leu Ser

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 gccttctgt cccgcgggaa gcggcaggag ccgccgccga cacctgaagg 150  
 aaaattgggc cgatttccac ctatgatgca tcatcaccag gcacctcag 200  
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 aagaggctctg atggggcaga ttattccaat ctacggtttt gggatttttt 350  
 tatatatact gtacattcta tttaaggtaa gtagaatcat cctaatacata 400  
 ttacatcaat gaaaatctaa tatggcgata aaaatcattg tctacattaa 450  
 aacttcttat agttcataaa attatttcaa atccatcatc tctttaaatc 500  
 ctgcctcttc ttcatgaggt acttaggata gccattattt cagtttcaca 550  
 taagaatggt tactcaatgt ttaagtgttt tgccccaaaa ttcacaacta 600  
 acaaggcaga actaggactt gaacatggat cttttggttc ttaatccagt 650  
 gagtgatata attcaatgca ctcccctgcc a 681

<210> 420  
 <211> 128  
 <212> PRT  
 <213> Homo sapiens

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 Gly Lys Arg Gln Glu Pro Pro Pro Thr Pro Glu Gly Lys Leu Gly  
 35 40 45

Arg Phe Pro Pro Met Met His His His Gln Ala Pro Ser Asp Gly  
50 55 60

Gln Thr Pro Gly Ala Arg Phe Gln Arg Ser His Leu Ala Glu Ala  
65 70 75

Phe Ala Lys Ala Lys Gly Ser Gly Gly Gly Ala Gly Gly Gly Gly  
80 85 90

Ser Gly Arg Gly Leu Met Gly Gln Ile Ile Pro Ile Tyr Gly Phe  
95 100 105

Gly Ile Phe Leu Tyr Ile Leu Tyr Ile Leu Phe Lys Val Ser Arg  
110 115 120

Ile Ile Leu Ile Ile Leu His Gln  
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aactcatcct gctgccagtg ttactggatt attccttggg cctgaatgac 150  
ttgaatgttt ccccgctga gtaacagtc catgtgggtg attcagctct 200  
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tgcaagaggc tgaccaggga acctatatct gtgaaatccg cctcaaaggg 450  
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caggatgtct gtggagtact ccagagctg gggccacttc cagaatcgtg 700  
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ctccccaata attgtacggg aggtgatcga ggaagaagaa ccaagtgaaa 1150  
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<211> 394  
<212> PRT  
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Thr Val His Val Gly Asp Ser Ala Leu Met Gly Cys Val Phe Gln  
35 40 45  
Ser Thr Glu Asp Lys Cys Ile Phe Lys Ile Asp Trp Thr Leu Ser  
50 55 60  
Pro Gly Glu His Ala Lys Asp Glu Tyr Val Leu Tyr Tyr Tyr Ser  
65 70 75  
Asn Leu Ser Val Pro Ile Gly Arg Phe Gln Asn Arg Val His Leu  
80 85 90  
Met Gly Asp Ile Leu Cys Asn Asp Gly Ser Leu Leu Leu Gln Asp  
95 100 105  
Val Gln Glu Ala Asp Gln Gly Thr Tyr Ile Cys Glu Ile Arg Leu  
110 115 120  
Lys Gly Glu Ser Gln Val Phe Lys Lys Ala Val Val Leu His Val  
125 130 135  
Leu Pro Glu Glu Pro Lys Glu Leu Met Val His Val Gly Gly Leu  
140 145 150  
Ile Gln Met Gly Cys Val Phe Gln Ser Thr Glu Val Lys His Val



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<210> 424  
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 <212> PRT  
 <213> Homo sapiens

<400> 424  
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 Arg Val Met Ala Leu Ile Leu Leu Ile Leu Cys Val Gly Met Val  
 35 40 45  
 Val Gly Leu Val Ala Leu Gly Ile Trp Ser Val Met Gln Arg Asn  
 50 55 60  
 Tyr Leu Gln Asp Glu Asn Glu Asn Arg Thr Gly Thr Leu Gln Gln  
 65 70 75  
 Leu Ala Lys Arg Phe Cys Gln Tyr Val Val Lys Gln Ser Glu Leu  
 80 85 90  
 Lys Gly Thr Phe Lys Gly His Lys Cys Ser Pro Cys Asp Thr Asn  
 95 100 105  
 Trp Arg Tyr Tyr Gly Asp Ser Cys Tyr Gly Phe Phe Arg His Asn  
 110 115 120  
 Leu Thr Trp Glu Glu Ser Lys Gln Tyr Cys Thr Asp Met Asn Ala

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Thr Leu Leu Lys	Ile Asp Asn Arg Asn	Ile Val Glu Tyr Ile	Lys		
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Ala Arg Thr His	Leu Ile Arg Trp Val	Gly Leu Ser Arg Gln	Lys		
	155	160	165		
Ser Asn Glu Val	Trp Lys Trp Glu Asp	Gly Ser Val Ile Ser	Glu		
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Asn Met Phe Glu	Phe Leu Glu Asp Gly	Lys Gly Asn Met Asn	Cys		
	185	190	195		
Ala Tyr Phe His	Asn Gly Lys Met His	Pro Thr Phe Cys Glu	Asn		
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<400> 426  
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<210> 428  
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<400> 434  
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<210> 435  
<211> 27  
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<400> 435  
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<400> 436  
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<210> 437  
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 <210> 464  
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 <211> 23  
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 <400> 468  
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<220>  
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 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 489  
 cagggccttc agggccttca c 21  
  
 <210> 490  
 <211> 19  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 490  
 gctcagccaa acactgtca 19  
  
 <210> 491  
 <211> 17  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 491  
 ggggcctga cagtgtt 17

<210> 492  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 492  
ctgagccgag actggagcat ctacac 26

<210> 493  
<211> 17  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 493  
gtgggcagcg tcttgct 17

<210> 494  
<211> 1231  
<212> DNA  
<213> Homo Sapien

<400> 494  
cccacgcgtc cgcgcagtcg cgcagttctg cctccgcctg ccagtctcgc 50  
ccgcgatccc ggcccggggc tgtggcgtcg actccgaccc aggcagccag 100  
cagcccgcgc gggagccgga ccgccgccgg aggagctcgg acggcatgct 150  
gagccccctc ctttgctgaa gcccgagtgc ggagaagccc gggcaaacgc 200  
aggctaagga gaccaaagcg gcgaagtcgc gagacagcgg acaagcagcg 250  
gaggagaagg aggaggaggc gaaccagag aggggcagca aaagaagcgg 300  
tggtggtggg cgtcgtggcc atggcgccgg ctatcgccag ctcgctcatc 350  
cgtcagaaga ggcaagcccg cgagcgcgag aaatccaacg cctgcaagtg 400  
tgtcagcagc cccagcaaag gcaagaccag ctgcgacaaa aacaagttaa 450  
atgtcttttc ccgggtcaaa ctcttcggct ccaagaagag gcgcagaaga 500  
agaccagagc ctcagcttaa ggttatagtt accaagctat acagccgaca 550  
aggctaccac ttgcagctgc aggcggatgg aaccattgat ggcaccaaag 600  
atgaggacag cacttacact ctgtttaacc tcatccctgt gggctctgca 650  
gtggtggcta tccaaggagt tcaaaccaag ctgtacttgg caatgaacag 700  
tgagggatac ttgtacacct cggaactttt cacacctgag tgcaaattca 750  
aagaatcagt gtttgaaaat tattatgtga catattcatc aatgatatac 800  
cgtcagcagc agtcaggccg agggtggtat ctgggtctga acaaagaagg 850  
agagatcatg aaaggcaacc atgtgaagaa gaacaagcct gcagctcatt 900



ttctgcctaa accactgaaa gtggccatgt acaaggagcc atcactgcac 950  
gatctcacgg agttctcccg atctggaagc gggaccccaa ccaagagcag 1000  
aagtgtctct ggcgtgctga acggaggcaa atccatgagc cacaatgaat 1050  
caacgtagcc agtgagggca aaagaagggc tctgtaacag aaccttacct 1100  
ccagggtgctg ttgaattctt ctagcagtc ttcacccaaa agttcaaatt 1150  
tgtcagtgac atttaccaaa caaacaggca gagttcacta ttctatctgc 1200  
cattagacct tcttatcatc cataactaaag c 1231

<210> 495  
<211> 245  
<212> PRT  
<213> Homo Sapien

<400> 495  
Met Ala Ala Ala Ile Ala Ser Ser Leu Ile Arg Gln Lys Arg Gln  
1 5 10 15  
Ala Arg Glu Arg Glu Lys Ser Asn Ala Cys Lys Cys Val Ser Ser  
20 25 30  
Pro Ser Lys Gly Lys Thr Ser Cys Asp Lys Asn Lys Leu Asn Val  
35 40 45  
Phe Ser Arg Val Lys Leu Phe Gly Ser Lys Lys Arg Arg Arg Arg  
50 55 60  
Arg Pro Glu Pro Gln Leu Lys Gly Ile Val Thr Lys Leu Tyr Ser  
65 70 75  
Arg Gln Gly Tyr His Leu Gln Leu Gln Ala Asp Gly Thr Ile Asp  
80 85 90  
Gly Thr Lys Asp Glu Asp Ser Thr Tyr Thr Leu Phe Asn Leu Ile  
95 100 105  
Pro Val Gly Leu Arg Val Val Ala Ile Gln Gly Val Gln Thr Lys  
110 115 120  
Leu Tyr Leu Ala Met Asn Ser Glu Gly Tyr Leu Tyr Thr Ser Glu  
125 130 135  
Leu Phe Thr Pro Glu Cys Lys Phe Lys Glu Ser Val Phe Glu Asn  
140 145 150  
Tyr Tyr Val Thr Tyr Ser Ser Met Ile Tyr Arg Gln Gln Gln Ser  
155 160 165  
Gly Arg Gly Trp Tyr Leu Gly Leu Asn Lys Glu Gly Glu Ile Met  
170 175 180  
Lys Gly Asn His Val Lys Lys Asn Lys Pro Ala Ala His Phe Leu  
185 190 195  
Pro Lys Pro Leu Lys Val Ala Met Tyr Lys Glu Pro Ser Leu His  
200 205 210  
Asp Leu Thr Glu Phe Ser Arg Ser Gly Ser Gly Thr Pro Thr Lys

	215		220		225
Ser Arg Ser Val Ser Gly Val Leu Asn Gly Gly Lys Ser Met Ser					
	230		235		240
His Asn Glu Ser Thr					
	245				

<210> 496  
 <211> 1471  
 <212> DNA  
 <213> Homo Sapien

<400> 496  
 ccaggatgga gctggggcct gtatagccat attattgttc tatgctacta 50  
 gacatggggg ggacttggtg aaaaaggtat tatccagcca gagggctctgg 100  
 gagccctgtc ttactgaacc tgggcaacct ggatattctg agacatattt 150  
 tggggggatt tcagtgaaaa aagtggggga tcccctccat ttagagtgtg 200  
 gcaaaggaaa aaacaccaag gttgggttcc ttctgacat tggcagtgcc 250  
 ccagtagggg tgggatgagc gaatattccc aaagctaaag tcccacaccc 300  
 tgtagattac aagagtggat ttggcaggag tgtgcccac aatacagtgg 350  
 aaaggtgcct gaagatattt aaaccacgtc ttggaaattt agtgggtctt 400  
 ggctttggga taggtgaagt gaggacagac actggagagg agggaaaggg 450  
 gacgttttca ataggaggca aaactcgagg gtgggatcca ctgaggagta 500  
 cataggctgc tggatctggt ggagccagca ctgggcccac ggggtggtaac 550  
 tggctgctgt ggaggggggt acgtgagggg ggggtctggg gcttatcctc 600  
 aggtcctgtg ggtggggcag cgagtcgggg cctgagcgtc aagagcatgc 650  
 cctagtgagc gggctcctct gggggagccc agcgcgctcc gggcgcctgc 700  
 cggtttgggg gtgtctcctc ccggggcgct atggcggcgc tggccagtag 750  
 cctgatccgg cagaagcggg aggtccgcga gcccgggggc agccggccgg 800  
 tgtcggcgca gcggcgcgtg tgtccccgcg gcaccaagtc cctttgccag 850  
 aagcagctcc tcctcctgct gtccaagggt cgactgtgcg gggggcggcc 900  
 cgcgcggccg gaccgcggcc cggagcctca gctcaaaggc atcgtcacca 950  
 aactgttctg ccgccagggt ttctacctcc aggcgaatcc cgacggaagc 1000  
 atccagggca ccccagagga taccagctcc ttcaccact tcaacctgat 1050  
 ccctgtgggc ctccgtgtgg tcaccatcca gagcgccaag ctgggtcact 1100  
 acatggccat gaatgctgag ggactgctct acagttcgcc gcatttcaca 1150  
 gctgagtgtc gctttaagga gtgtgtcttt gagaattact acgtcctgta 1200  
 cgcctctgct ctctaccgcc agcgtcgttc tggccggggc tggtagctcg 1250

gcctggacaa ggagggccag gtcatgaagg gaaaccgagt taagaagacc 1300  
aaggcagctg cccactttct gccaagctc ctggaggtgg ccatgtacca 1350  
ggagccttct ctccacagtg tccccgaggc ctccccttcc agtccccctg 1400  
ccccctgaaa tgtagtccct ggactggagg ttccctgcac tcccagtga 1450  
ccagccacca ccacaacctg t 1471

<210> 497  
<211> 225  
<212> PRT  
<213> Homo Sapien

<400> 497  
Met Ala Ala Leu Ala Ser Ser Leu Ile Arg Gln Lys Arg Glu Val  
1 5 10 15  
Arg Glu Pro Gly Gly Ser Arg Pro Val Ser Ala Gln Arg Arg Val  
20 25 30  
Cys Pro Arg Gly Thr Lys Ser Leu Cys Gln Lys Gln Leu Leu Ile  
35 40 45  
Leu Leu Ser Lys Val Arg Leu Cys Gly Gly Arg Pro Ala Arg Pro  
50 55 60  
Asp Arg Gly Pro Glu Pro Gln Leu Lys Gly Ile Val Thr Lys Leu  
65 70 75  
Phe Cys Arg Gln Gly Phe Tyr Leu Gln Ala Asn Pro Asp Gly Ser  
80 85 90  
Ile Gln Gly Thr Pro Glu Asp Thr Ser Ser Phe Thr His Phe Asn  
95 100 105  
Leu Ile Pro Val Gly Leu Arg Val Val Thr Ile Gln Ser Ala Lys  
110 115 120  
Leu Gly His Tyr Met Ala Met Asn Ala Glu Gly Leu Leu Tyr Ser  
125 130 135  
Ser Pro His Phe Thr Ala Glu Cys Arg Phe Lys Glu Cys Val Phe  
140 145 150  
Glu Asn Tyr Tyr Val Leu Tyr Ala Ser Ala Leu Tyr Arg Gln Arg  
155 160 165  
Arg Ser Gly Arg Ala Trp Tyr Leu Gly Leu Asp Lys Glu Gly Gln  
170 175 180  
Val Met Lys Gly Asn Arg Val Lys Lys Thr Lys Ala Ala Ala His  
185 190 195  
Phe Leu Pro Lys Leu Leu Glu Val Ala Met Tyr Gln Glu Pro Ser  
200 205 210  
Leu His Ser Val Pro Glu Ala Ser Pro Ser Ser Pro Pro Ala Pro  
215 220 225

<210> 498  
<211> 744

<212> DNA  
 <213> Homo Sapien

<400> 498  
 atggccgcgg coactcgctag cggcttgatc cgccagaagc ggcaggcgcg 50  
 ggagcagcac tgggaccggc cgtctgccag caggaggcgg agcagcccca 100  
 gcaagaaccg cgggctctgc aacggcaacc tgggtggatat cttctccaaa 150  
 gtgcgcactct tgggcctcaa gaagcgcagg ttgcgggcgcc aagatcccca 200  
 gctcaagggg atagtgacca ggttatattg caggcaaggc tactacttgc 250  
 aaatgcaccc cgatggagct ctcgatggaa ccaaggatga cagcactaat 300  
 tctacactct tcaacctcat accagtggga ctacgtgttg ttgccatcca 350  
 gggagtgaaa acagggttgt atatagccat gaatggagaa ggttacctct 400  
 acccatcaga actttttacc cctgaatgca agtttaaaga atctgttttt 450  
 gaaaattatt atgtaatcta ctcatccatg ttgtacagac aacaggaatc 500  
 tggtagagcc tggtttttgg gattaaataa ggaagggcaa gctatgaaag 550  
 ggaacagagt aaagaaaacc aaaccagcag ctcatcttct acccaagcca 600  
 ttggaagttg ccatgtaccg agaaccatct ttgcatgatg ttggggaaac 650  
 ggtcccgaa cctgggggtga cgccaagtaa aagcacaagt gcgtctgcaa 700  
 taatgaatgg aggcaaacca gtcaacaaga gtaagacaac atag 744

<210> 499  
 <211> 247  
 <212> PRT  
 <213> Homo Sapien

<400> 499  
 Met Ala Ala Ala Ile Ala Ser Gly Leu Ile Arg Gln Lys Arg Gln  
 1 5 10 15  
 Ala Arg Glu Gln His Trp Asp Arg Pro Ser Ala Ser Arg Arg Arg  
 20 25 30  
 Ser Ser Pro Ser Lys Asn Arg Gly Leu Cys Asn Gly Asn Leu Val  
 35 40 45  
 Asp Ile Phe Ser Lys Val Arg Ile Phe Gly Leu Lys Lys Arg Arg  
 50 55 60  
 Leu Arg Arg Gln Asp Pro Gln Leu Lys Gly Ile Val Thr Arg Leu  
 65 70 75  
 Tyr Cys Arg Gln Gly Tyr Tyr Leu Gln Met His Pro Asp Gly Ala  
 80 85 90  
 Leu Asp Gly Thr Lys Asp Asp Ser Thr Asn Ser Thr Leu Phe Asn  
 95 100 105  
 Leu Ile Pro Val Gly Leu Arg Val Val Ala Ile Gln Gly Val Lys  
 110 115 120

Thr	Gly	Leu	Tyr	Ile	Ala	Met	Asn	Gly	Glu	Gly	Tyr	Leu	Tyr	Pro	125	130	135
Ser	Glu	Leu	Phe	Thr	Pro	Glu	Cys	Lys	Phe	Lys	Glu	Ser	Val	Phe	140	145	150
Glu	Asn	Tyr	Tyr	Val	Ile	Tyr	Ser	Ser	Met	Leu	Tyr	Arg	Gln	Gln	155	160	165
Glu	Ser	Gly	Arg	Ala	Trp	Phe	Leu	Gly	Leu	Asn	Lys	Glu	Gly	Gln	170	175	180
Ala	Met	Lys	Gly	Asn	Arg	Val	Lys	Lys	Thr	Lys	Pro	Ala	Ala	His	185	190	195
Phe	Leu	Pro	Lys	Pro	Leu	Glu	Val	Ala	Met	Tyr	Arg	Glu	Pro	Ser	200	205	210
Leu	His	Asp	Val	Gly	Glu	Thr	Val	Pro	Lys	Pro	Gly	Val	Thr	Pro	215	220	225
Ser	Lys	Ser	Thr	Ser	Ala	Ser	Ala	Ile	Met	Asn	Gly	Gly	Lys	Pro	230	235	240
Val	Asn	Lys	Ser	Lys	Thr	Thr									245		

<210> 500  
 <211> 2906  
 <212> DNA  
 <213> Homo Sapien

<400> 500  
 ggggagagga attgaccatg taaaaggaga cttttttttt tgggtggtggt 50  
 ggctgttggtg tgccttgcaa aaatgaagga tgcaggacgc agctttctcc 100  
 tggaaccgaa cgcaatggat aaactgattg tgcaagagag aaggaagaac 150  
 gaagcttttt cttgtgagcc ctggatctta acacaaatgt gtatatgtgc 200  
 acacagggag cattcaagaa tgaaataaac cagagttaga cccgcggggg 250  
 ttggtgtggt ctgacataaa taaataatct taaagcagct gttcccctcc 300  
 ccacccccaa aaaaaaggat gattggaaat gaagaaccga ggattcacia 350  
 agaaaaaagt atgttcattt ttctctataa aggagaaagt gagccaagga 400  
 gatatttttg gaatgaaaag tttggggcct ttttagtaaa gtaaagaact 450  
 ggtgtggtggt tgttttcctt tctttttgaa tttcccacia gaggagagga 500  
 aattaataat acatctgcaa agaaatttca gagaagaaaa gttgaccgcg 550  
 gcagattgag gcattgattg ggggagagaa accagcagag cacagttgga 600  
 tttgtgccta tgttgactaa aattgacgga taattgcagt tggatttttc 650  
 ttcatacaacc tcottttttt taaattttta ttccttttgg tatcaagatc 700  
 atgcgttttc tcttgttctt aaccacctgg atttccatct ggatgttgct 750

gtgatcagtc tgaaatacaa ctgtttgaat tccagaagga ccaacaccag 800  
ataaattatg aatgttgaac aagatgacct tacatccaca gcagataatg 850  
ataggtocta ggtttaacag ggccctatct gacccctgc ttgtggtgct 900  
gctggctctt caacttcttg tgggtgctgg tctggtgcgg gctcagacct 950  
gcccttctgt gtgctcctgc agcaaccagt tcagcaaggt gatttgtgtt 1000  
cggaaaaacc tgcgtgaggt tccggatggc atctccacca acacacggct 1050  
gctgaacctc catgagaacc aaatccagat catcaaagt aacagcttca 1100  
agcacttgag gcacttgga atcctacagt tgagttagaa ccatatcaga 1150  
accattgaaa ttggggcttt caatggtctg gcgaacctca acactctgga 1200  
actctttgac aatcgtctta ctaccatccc gaatggagct tttgtatact 1250  
tgtctaaact gaaggagctc tgggtgcga acaaccccat tgaaagcatc 1300  
ccttcttatg cttttaacag aattccttct ttgcgcgcac tagacttagg 1350  
ggaattgaaa agactttcat acatctcaga aggtgccttt gaaggctctgt 1400  
ccaacttgag gtatttgaac ctggccatgt gcaaccttcg ggaaatccct 1450  
aacctcacac cgctcataaa actagatgag ctggatcttt ctgggaatca 1500  
tttatctgcc atcaggcctg gctctttcca gggtttgatg caccttcaaa 1550  
aactgtggat gatacagtc cagattcaag tgattgaacg gaatgccttt 1600  
gacaaccttc agtcactagt ggagatcaac ctggcacaca ataactaac 1650  
attactgcct catgacctct tcaactccct gcacatcta gagcggatac 1700  
atttacatca caaccttg aactgtaact gtgacatact gtggctcagc 1750  
tggtgagataa aagacatggc cccctcgaac acagcttggt gtgcccgggtg 1800  
taacactcct cccaatctaa aggggaggt cattggagag ctcgaccaga 1850  
attacttcac atgctatgct ccggtgattg tggagcccc tgcagacctc 1900  
aatgtcactg aaggcatggc agctgagctg aaatgtcggg cctccacatc 1950  
cctgacatct gtatcttgga ttactccaaa tggaacagtc atgacacatg 2000  
gggcgtacaa agtgccgata gctgtgctca gtgatggtac gttaaatttc 2050  
acaaatgtaa ctgtgcaaga tacaggcatg tacacatgta tggtagtaaa 2100  
ttccgttggg aatactactg cttcagccac cctgaatggt actgcagcaa 2150  
ccactactcc tttctcttac ttttcaaccg tcacagtaga gactatggaa 2200  
ccgtctcagg atgaggcacg gaccacagat aacaatgtgg gtccactcc 2250  
agtggctcag tgggagacca ccaatgtgac cacctctctc acaccacaga 2300  
gcacaaggct gacagagaaa accttcacca tcccagtgac tgatataaac 2350

agtgggatcc caggaattga tgaggatcatg aagactacca aaatcatcat 2400  
 tgggtgtttt gtggccatca cactcatggc tgcagtgatg ctggtcattt 2450  
 tctacaagat gaggaagcag caccatcggc aaaaccatca cgccccaaca 2500  
 aggactgttg aaattattaa tgtggatgat gagattacgg gagacacacc 2550  
 catggaaagc cacctgcca tgctgtctat cgagcatgag cacctaaatc 2600  
 actataactc atacaaatct cccttcaacc acacaacaac agttaacaca 2650  
 ataaattcaa tacacagttc agtgcagtga cgtttattga tccgaatgaa 2700  
 ctctaaagac aatgtacaag agactcaa ataaaacatt tacagagtta 2750  
 caaaaaacaa acaatcaaaa aaaaagacag tttattaaaa atgacacaaa 2800  
 tgactgggct aaatctactg tttcaaaaaa gtgtctttac aaaaaacaa 2850  
 aaaagaaaag aaatttattt attaaaaatt ctattgtgat ctaaagcaga 2900  
 caaaaa 2906

<210> 501  
 <211> 640  
 <212> PRT  
 <213> Homo Sapien

<400> 501  
 Met Leu Asn Lys Met Thr Leu His Pro Gln Gln Ile Met Ile Gly  
 1 5 10 15  
 Pro Arg Phe Asn Arg Ala Leu Phe Asp Pro Leu Leu Val Val Leu  
 20 25 30  
 Leu Ala Leu Gln Leu Leu Val Val Ala Gly Leu Val Arg Ala Gln  
 35 40 45  
 Thr Cys Pro Ser Val Cys Ser Cys Ser Asn Gln Phe Ser Lys Val  
 50 55 60  
 Ile Cys Val Arg Lys Asn Leu Arg Glu Val Pro Asp Gly Ile Ser  
 65 70 75  
 Thr Asn Thr Arg Leu Leu Asn Leu His Glu Asn Gln Ile Gln Ile  
 80 85 90  
 Ile Lys Val Asn Ser Phe Lys His Leu Arg His Leu Glu Ile Leu  
 95 100 105  
 Gln Leu Ser Arg Asn His Ile Arg Thr Ile Glu Ile Gly Ala Phe  
 110 115 120  
 Asn Gly Leu Ala Asn Leu Asn Thr Leu Glu Leu Phe Asp Asn Arg  
 125 130 135  
 Leu Thr Thr Ile Pro Asn Gly Ala Phe Val Tyr Leu Ser Lys Leu  
 140 145 150  
 Lys Glu Leu Trp Leu Arg Asn Asn Pro Ile Glu Ser Ile Pro Ser  
 155 160 165

Tyr	Ala	Phe	Asn	Arg 170	Ile	Pro	Ser	Leu	Arg 175	Arg	Leu	Asp	Leu	Gly 180
Glu	Leu	Lys	Arg	Leu 185	Ser	Tyr	Ile	Ser	Glu 190	Gly	Ala	Phe	Glu	Gly 195
Leu	Ser	Asn	Leu	Arg 200	Tyr	Leu	Asn	Leu	Ala 205	Met	Cys	Asn	Leu	Arg 210
Glu	Ile	Pro	Asn	Leu 215	Thr	Pro	Leu	Ile	Lys 220	Leu	Asp	Glu	Leu	Asp 225
Leu	Ser	Gly	Asn	His 230	Leu	Ser	Ala	Ile	Arg 235	Pro	Gly	Ser	Phe	Gln 240
Gly	Leu	Met	His	Leu 245	Gln	Lys	Leu	Trp	Met 250	Ile	Gln	Ser	Gln	Ile 255
Gln	Val	Ile	Glu	Arg 260	Asn	Ala	Phe	Asp	Asn 265	Leu	Gln	Ser	Leu	Val 270
Glu	Ile	Asn	Leu	Ala 275	His	Asn	Asn	Leu	Thr 280	Leu	Leu	Pro	His	Asp 285
Leu	Phe	Thr	Pro	Leu 290	His	His	Leu	Glu	Arg 295	Ile	His	Leu	His	His 300
Asn	Pro	Trp	Asn	Cys 305	Asn	Cys	Asp	Ile	Leu 310	Trp	Leu	Ser	Trp	Trp 315
Ile	Lys	Asp	Met	Ala 320	Pro	Ser	Asn	Thr	Ala 325	Cys	Cys	Ala	Arg	Cys 330
Asn	Thr	Pro	Pro	Asn 335	Leu	Lys	Gly	Arg	Tyr 340	Ile	Gly	Glu	Leu	Asp 345
Gln	Asn	Tyr	Phe	Thr 350	Cys	Tyr	Ala	Pro	Val 355	Ile	Val	Glu	Pro	Pro 360
Ala	Asp	Leu	Asn	Val 365	Thr	Glu	Gly	Met	Ala 370	Ala	Glu	Leu	Lys	Cys 375
Arg	Ala	Ser	Thr	Ser 380	Leu	Thr	Ser	Val	Ser 385	Trp	Ile	Thr	Pro	Asn 390
Gly	Thr	Val	Met	Thr 395	His	Gly	Ala	Tyr	Lys 400	Val	Arg	Ile	Ala	Val 405
Leu	Ser	Asp	Gly	Thr 410	Leu	Asn	Phe	Thr	Asn 415	Val	Thr	Val	Gln	Asp 420
Thr	Gly	Met	Tyr	Thr 425	Cys	Met	Val	Ser	Asn 430	Ser	Val	Gly	Asn	Thr 435
Thr	Ala	Ser	Ala	Thr 440	Leu	Asn	Val	Thr	Ala 445	Ala	Thr	Thr	Thr	Pro 450
Phe	Ser	Tyr	Phe	Ser 455	Thr	Val	Thr	Val	Glu 460	Thr	Met	Glu	Pro	Ser 465
Gln	Asp	Glu	Ala	Arg 470	Thr	Thr	Asp	Asn	Asn 475	Val	Gly	Pro	Thr	Pro 480



Val	Val	Asp	Trp	Glu	Thr	Thr	Asn	Val	Thr	Thr	Ser	Leu	Thr	Pro
				485					490					495
Gln	Ser	Thr	Arg	Ser	Thr	Glu	Lys	Thr	Phe	Thr	Ile	Pro	Val	Thr
				500					505					510
Asp	Ile	Asn	Ser	Gly	Ile	Pro	Gly	Ile	Asp	Glu	Val	Met	Lys	Thr
				515					520					525
Thr	Lys	Ile	Ile	Ile	Gly	Cys	Phe	Val	Ala	Ile	Thr	Leu	Met	Ala
				530					535					540
Ala	Val	Met	Leu	Val	Ile	Phe	Tyr	Lys	Met	Arg	Lys	Gln	His	His
				545					550					555
Arg	Gln	Asn	His	His	Ala	Pro	Thr	Arg	Thr	Val	Glu	Ile	Ile	Asn
				560					565					570
Val	Asp	Asp	Glu	Ile	Thr	Gly	Asp	Thr	Pro	Met	Glu	Ser	His	Leu
				575					580					585
Pro	Met	Pro	Ala	Ile	Glu	His	Glu	His	Leu	Asn	His	Tyr	Asn	Ser
				590					595					600
Tyr	Lys	Ser	Pro	Phe	Asn	His	Thr	Thr	Thr	Val	Asn	Thr	Ile	Asn
				605					610					615
Ser	Ile	His	Ser	Ser	Val	His	Glu	Pro	Leu	Leu	Ile	Arg	Met	Asn
				620					625					630
Ser	Lys	Asp	Asn	Val	Gln	Glu	Thr	Gln	Ile					
				635					640					

<210> 502  
 <211> 2458  
 <212> DNA  
 <213> Homo Sapien

<400> 502  
 gcgccgggag cccatctgcc ccagggggca cggggcgcg ggccggctcc 50  
 cgcccggcac atggctgcag ccacctcgcg cgcaccccg ggccggcgcg 100  
 ccagctcgcc cgaggtccgt cggagggcgcc cggccgcccc ggagccaagc 150  
 agcaactgag cggggaagcg cccgcgtccg gggatcgga tgtccctcct 200  
 ctttctctc ttgctagttt cctactatgt tggaaccttg gggactcaca 250  
 ctgagatcaa gagagtggca gaggaaaagg tcactttgcc ctgccacat 300  
 caactggggc ttccagaaaa agacactctg gatattgaat ggctgctcac 350  
 cgataatgaa gggaacaaaa aagtggatgat cacttactcc agtcgtcatg 400  
 tctacaataa cttgaactgag gaacagaagg gccgagtggc ctttgcttcc 450  
 aatttctgag caggagatgc ctccttgag attgaacctc tgaagcccag 500  
 tgatgagggc cggtagacct gtaagggtta gaattcaggg cgctacgtgt 550  
 ggagccatgt catcttaaaa gtcttagtga gaccatcaa gcccaagtgt 600

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 aaccaccctg gacgagttct gctgcagaat cttaccatgt cctactctgg 800  
 actgtaccag tgcacagcag gcaacgaagc tgggaaggaa agctgtgtgg 850  
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 ccagaggtga gaggttctga accaaagaaa gtccaccatg ctaactctgac 1250  
 caaagcagaa accacaccca gcatgatccc cagccagagc agagccttcc 1300  
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 gggctcttgg actcttctcg tcattggagc tcaagtcacc agccacacaa 1400  
 ccagatgaga ggtcatctaa gtagcagtga gcattgcacg gaacagattc 1450  
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 gattcatctg taaaaaggca tcttattgtg ctttagacc agagtaaggg 1550  
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 aatttgtgac aaaggattgt gaagagcttt ccatcttcat gatgttatga 2050  
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 cgggcatggg gccaggcacc tgtaggaaaa tccagcaggt ggaggttgca 2400  
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 tccgtctc 2458

<210> 503  
 <211> 373  
 <212> PRT  
 <213> Homo Sapien

<400> 503  
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 20 25 30  
 Val Thr Leu Pro Cys His His Gln Leu Gly Leu Pro Glu Lys Asp  
 35 40 45  
 Thr Leu Asp Ile Glu Trp Leu Leu Thr Asp Asn Glu Gly Asn Gln  
 50 55 60  
 Lys Val Val Ile Thr Tyr Ser Ser Arg His Val Tyr Asn Asn Leu  
 65 70 75  
 Thr Glu Glu Gln Lys Gly Arg Val Ala Phe Ala Ser Asn Phe Leu  
 80 85 90  
 Ala Gly Asp Ala Ser Leu Gln Ile Glu Pro Leu Lys Pro Ser Asp  
 95 100 105  
 Glu Gly Arg Tyr Thr Cys Lys Val Lys Asn Ser Gly Arg Tyr Val  
 110 115 120  
 Trp Ser His Val Ile Leu Lys Val Leu Val Arg Pro Ser Lys Pro  
 125 130 135  
 Lys Cys Glu Leu Glu Gly Glu Leu Thr Glu Gly Ser Asp Leu Thr  
 140 145 150  
 Leu Gln Cys Glu Ser Ser Ser Gly Thr Glu Pro Ile Val Tyr Tyr  
 155 160 165  
 Trp Gln Arg Ile Arg Glu Lys Glu Gly Glu Asp Glu Arg Leu Pro  
 170 175 180  
 Pro Lys Ser Arg Ile Asp Tyr Asn His Pro Gly Arg Val Leu Leu  
 185 190 195  
 Gln Asn Leu Thr Met Ser Tyr Ser Gly Leu Tyr Gln Cys Thr Ala  
 200 205 210  
 Gly Asn Glu Ala Gly Lys Glu Ser Cys Val Val Arg Val Thr Val  
 215 220 225

Gln Tyr Val Gln Ser Ile Gly Met Val Ala Gly Ala Val Thr Gly  
 230 235 240  
 Ile Val Ala Gly Ala Leu Leu Ile Phe Leu Leu Val Trp Leu Leu  
 245 250 255  
 Ile Arg Arg Lys Asp Lys Glu Arg Tyr Glu Glu Glu Glu Arg Pro  
 260 265 270  
 Asn Glu Ile Arg Glu Asp Ala Glu Ala Pro Lys Ala Arg Leu Val  
 275 280 285  
 Lys Pro Ser Ser Ser Ser Ser Gly Ser Arg Ser Ser Arg Ser Gly  
 290 295 300  
 Ser Ser Ser Thr Arg Ser Thr Ala Asn Ser Ala Ser Arg Ser Gln  
 305 310 315  
 Arg Thr Leu Ser Thr Asp Ala Ala Pro Gln Pro Gly Leu Ala Thr  
 320 325 330  
 Gln Ala Tyr Ser Leu Val Gly Pro Glu Val Arg Gly Ser Glu Pro  
 335 340 345  
 Lys Lys Val His His Ala Asn Leu Thr Lys Ala Glu Thr Thr Pro  
 350 355 360  
 Ser Met Ile Pro Ser Gln Ser Arg Ala Phe Gln Thr Val  
 365 370

<210> 504  
 <211> 3060  
 <212> DNA  
 <213> Homo Sapien

<400> 504  
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 ctctgtgctg gagtagtgga tttcgccaga agtttgagta tcactactcc 150  
 tgaagagatg attgaaaaag ccaaagggga aactgcctat ctgocatgca 200  
 aatttacgct tagtcccgaa gaccagggac cgctggacat cgagtggctg 250  
 atatcaccag ctgataatca gaaggtggat caagtgatta ttttatattc 300  
 tggagacaaa atttatgatg actactatcc agatctgaaa ggccgagtac 350  
 attttacgag taatgatctc aaatctgggtg atgcatcaat aaatgtaacg 400  
 aatttacaac tgtcagatat tggcacatat cagtgc aaag tgaaaaaagc 450  
 tcctggtggt gcaaataaga agattcatct ggtagttctt gtttaagcctt 500  
 caggtgctgag atgttacgtt gatggatctg aagaaattgg aagtgacttt 550  
 aagataaaat gtgaacccaaa agaaggttca cttccattac agtatgagtg 600  
 gcaaaaattg tctgactcac agaaaatgcc cacttcattg ttagcagaaa 650  
 tgacttcac tggtatatct gtaaaaaatg cctcttctga gtactctggg 700

acatacagct gtacagtcag aaacagagtg ggctctgatc agtgccctgtt 750  
 gcgtctaaac gttgtccctc cttcaaataa agctggacta attgcaggag 800  
 ccattatagg aacttttgctt gctctagcgc tcattggtct tatcatcttt 850  
 tgctgtcgtt aaaagcgcag agaagaaaaa tatgaaaagg aagttcatca 900  
 cgatatcagg gaagatgtgc cacctccaaa gagccgtacg tccactgcca 950  
 gaagctacat cggcagtaat cattcatccc tgggggtccat gtctccttcc 1000  
 aacatggaag gatattccaa gactcagtat aaccaagtac caagtgaaga 1050  
 ctttgaacgc actcctcaga gtccgactct cccacctgct aagttcaagt 1100  
 acccttaciaa gactgatgga attacagttg tataaatatg gactactgaa 1150  
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 cttaaatgtt ttttaaaaaa agcacaaggc acagagatta gagcagctgt 1250  
 aagaacacat ctactttatg caatggcatt agacatgtaa gtcagatgtc 1300  
 atgtcaaaat tagtacgagc caaattcttt gttaaaaaac cctatgtata 1350  
 gtgacactga tagttaaaaag atgttttatt atattttcaa taactaccac 1400  
 taacaaatth ttaacttttc atatgcatat tctgatatgt ggtcttttag 1450  
 gaaaagtatg gttaatagtt gatttttcaa aggaaattht aaaattctta 1500  
 cgttctgttt aatgtttttg ctatttagtt aaatacattg aagggaata 1550  
 cccgttcttt tcccctttta tgcacacaac agaaacacgc gttgtcatgc 1600  
 ctcaaactat tttttatttg caactacatg atttcacaca attctcttaa 1650  
 acaacgacat aaaatagatt tcottgtata taaataactt acatacgctc 1700  
 cataaagtaa attctcaaag gtgctagaac aaatcgtcca cttctacagt 1750  
 gttctcgtat ccaacagagt tgatgcacaa tatataaata ctcaagtcca 1800  
 atattaaaaa cttaggcact tgactaactt taataaaaatt tctcaacta 1850  
 tatcaatata taaagtgcatt atatttttta agaaagatta ttctcaataa 1900  
 cttctataaa aataagtttg atggtttggc ccatctaact tcaactactat 1950  
 tagtaagaac ttttaacttt taatgtgtag taaggtttat totacctttt 2000  
 totcaacatg acaccaacac aatcaaaaac gaagttagtg aggtgctaac 2050  
 atgtgaggat taatccagtg attccggtca caatgcattc caggaggagg 2100  
 taccatgtc actggaattg ggcgatatgg tttatttttt cttccctgat 2150  
 ttggataacc aaatggaaca ggaggaggat agtgattctg atggccattc 2200  
 cctcgatata ttcttggtt ttttctgggc aaagggtgcc acattggaag 2250  
 aggtggaaat ataagttctg aaatctgtag ggaagagaac acattaagtt 2300



	125		130		135
Val Val Leu Val	Lys Pro Ser Gly Ala	Arg Cys Tyr Val Asp Gly			
	140	145			150
Ser Glu Glu Ile	Gly Ser Asp Phe Lys	Ile Lys Cys Glu Pro Lys			
	155	160			165
Glu Gly Ser Leu	Pro Leu Gln Tyr Glu	Trp Gln Lys Leu Ser Asp			
	170	175			180
Ser Gln Lys Met	Pro Thr Ser Trp Leu	Ala Glu Met Thr Ser Ser			
	185	190			195
Val Ile Ser Val	Lys Asn Ala Ser Ser	Glu Tyr Ser Gly Thr Tyr			
	200	205			210
Ser Cys Thr Val	Arg Asn Arg Val Gly	Ser Asp Gln Cys Leu Leu			
	215	220			225
Arg Leu Asn Val	Val Pro Pro Ser Asn	Lys Ala Gly Leu Ile Ala			
	230	235			240
Gly Ala Ile Ile	Gly Thr Leu Leu Ala	Leu Ala Leu Ile Gly Leu			
	245	250			255
Ile Ile Phe Cys	Cys Arg Lys Lys Arg	Arg Glu Glu Lys Tyr Glu			
	260	265			270
Lys Glu Val His	His Asp Ile Arg Glu	Asp Val Pro Pro Pro Lys			
	275	280			285
Ser Arg Thr Ser	Thr Ala Arg Ser Tyr	Ile Gly Ser Asn His Ser			
	290	295			300
Ser Leu Gly Ser	Met Ser Pro Ser Asn	Met Glu Gly Tyr Ser Lys			
	305	310			315
Thr Gln Tyr Asn	Gln Val Pro Ser Glu	Asp Phe Glu Arg Thr Pro			
	320	325			330
Gln Ser Pro Thr	Leu Pro Pro Ala Lys	Phe Lys Tyr Pro Tyr Lys			
	335	340			345
Thr Asp Gly Ile	Thr Val Val				
	350				

<210> 506  
 <211> 1705  
 <212> DNA  
 <213> Homo Sapien

<400> 506  
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 ccagctgcct ccaggcagcc agccctcaag catcacttac aggaccagag 150  
 ggacaagaca tgactgtgat gaggagctgc tttcgccaat ttaacaccaa 200  
 gaagaattga ggctgcttgg gaggaaggcc aggaggaaca cgagactgag 250

agatgaatTT tcaacagagg ctgcaaagcc tgtggactTT agccagaccc 300  
 ttctgccctc ctttgctggc gacagcctct caaatgcaga tggttgtgct 350  
 cccttgccctg ggtttttacc tgcttctctg gagccaggta tcagggggccc 400  
 agggccaaga attccactTT gggccctgcc aagtgaaggg ggttgttccc 450  
 cagaaactgt gggaagcctt ctgggctgtg aaagacacta tgcaagctca 500  
 ggataacatc acgagtggcc ggctgctgca gcaggagggt ctgcagaacg 550  
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 ttgaaaactg ttttcaaaaa ccaccacaat agaacagttg aagtcaggac 650  
 tctgaagtca ttctctactc tggccaacaa ctttgttctc atcgtgtcac 700  
 aactgcaacc cagtcaagaa aatgagatgt tttccatcag agacagtgc 750  
 cacaggcggT ttctgctatt ccggagagca ttcaaacagt tggacgtaga 800  
 agcagctctg accaaagccc ttggggaagt ggacattctt ctgacctgga 850  
 tgcagaaatt ctacaagctc tgaatgtota gaccaggacc tccctcccc 900  
 tggcactggT ttgttccctg tgtcatttca aacagtctcc cttcctatgc 950  
 tgttcactgg acacttcacg cccttggcca tgggtcccat tcttggccca 1000  
 ggattattgt caaagaagtc attctttaag cagcgccagt gacagtcagg 1050  
 gaaggtgcct ctggatgctg tgaagagtct acagagaaga ttcttgtatt 1100  
 tattacaact ctatttaatt aatgtcagta tttcaactga agttctattt 1150  
 atttgtgaga ctgtaagtta catgaaggca gcagaatatt gtgccccatg 1200  
 cttctttacc cctcacaatc cttgccacag tgtggggcag tggatgggtg 1250  
 cttagtaagt acttaataaa ctgtggtgct ttttttggcc tgtctttgga 1300  
 ttgttaaaaa acagagaggg atgcttggat gtaaaactga acttcagagc 1350  
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 ggggtaaggT gcatctgttt gaaaagtaaa cgataaaatg tggattaaag 1450  
 tgcccagcac aaagcagatc ctcaataaac atttcatttc ccaccacac 1500  
 tcgccagctc accccatcat ccctttccct tggtgccctc cttttttttt 1550  
 tatcctagtc attcttccct aatcttcac ttgagtgtca agctgacctt 1600  
 gctgatgggtg acattgcacc tggatgtact atccaatctg tgatgacatt 1650  
 ccctgctaatt aaaagacaac ataactcaa aaaaaaaaaa aaaaaaaaaa 1700  
 aaaaa 1705

<210> 507  
 <211> 206  
 <212> PRT



<213> Homo Sapien

<400> 507

Met Asn Phe Gln Gln Arg Leu Gln Ser Leu Trp Thr Leu Ala Arg  
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Pro Phe Cys Pro Pro Leu Leu Ala Thr Ala Ser Gln Met Gln Met  
20 25 30  
Val Val Leu Pro Cys Leu Gly Phe Thr Leu Leu Leu Trp Ser Gln  
35 40 45  
Val Ser Gly Ala Gln Gly Gln Glu Phe His Phe Gly Pro Cys Gln  
50 55 60  
Val Lys Gly Val Val Pro Gln Lys Leu Trp Glu Ala Phe Trp Ala  
65 70 75  
Val Lys Asp Thr Met Gln Ala Gln Asp Asn Ile Thr Ser Ala Arg  
80 85 90  
Leu Leu Gln Gln Glu Val Leu Gln Asn Val Ser Asp Ala Glu Ser  
95 100 105  
Cys Tyr Leu Val His Thr Leu Leu Glu Phe Tyr Leu Lys Thr Val  
110 115 120  
Phe Lys Asn His His Asn Arg Thr Val Glu Val Arg Thr Leu Lys  
125 130 135  
Ser Phe Ser Thr Leu Ala Asn Asn Phe Val Leu Ile Val Ser Gln  
140 145 150  
Leu Gln Pro Ser Gln Glu Asn Glu Met Phe Ser Ile Arg Asp Ser  
155 160 165  
Ala His Arg Arg Phe Leu Leu Phe Arg Arg Ala Phe Lys Gln Leu  
170 175 180  
Asp Val Glu Ala Ala Leu Thr Lys Ala Leu Gly Glu Val Asp Ile  
185 190 195  
Leu Leu Thr Trp Met Gln Lys Phe Tyr Lys Leu  
200 205

<210> 508

<211> 924

<212> DNA

<213> Homo Sapien

<400> 508

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cgggtctcagg agatgtctga tttccacaga catgcacat atagaagaga 150  
gtttccaaga aatcaaaaga gccatccaag ctaaggacac cttcccaa 200  
gtcactatcc tgtccacatt ggagactctg cagatcatta agcccttaga 250  
tgtgtgtgtgc gtgaccaaga acctcctggc gttctacgtg gacagggtgt 300

tcaaggatca tcaggagcca aacccccaaaa tcttgagaaa aatcagcagc 350  
attgccaaact ctttctctta catgcagaaa actctgcggc aatgtcagga 400  
acagaggcag tgtcactgca ggcaggaagc caccaatgcc accagagtca 450  
tccatgacaa ctatgatcag ctggaggtcc acgctgctgc cattaaatcc 500  
ctgggagagc tcgacgtctt tctagcctgg attaataaga atcatgaagt 550  
aatgtttctca gcttgatgac aaggaacctg tatagtgatc cagggatgaa 600  
caccctctgt gcggtttact gtgggagaca gccaccttg aagggaagg 650  
agatggggaa ggcccttgcc agctgaaagt cccactggct ggccctcaggc 700  
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tgccttccca tctaatttat tgtaaagtca tatagtccat gtctgtgatg 850  
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ataaattcca tattttacct atga 924

<210> 509

<211> 177

<212> PRT

<213> Homo Sapien

<400> 509

Met	Lys	Leu	Gln	Cys	Val	Ser	Leu	Trp	Leu	Leu	Gly	Thr	Ile	Leu	1	5	10	15
Ile	Leu	Cys	Ser	Val	Asp	Asn	His	Gly	Leu	Arg	Arg	Cys	Leu	Ile	20	25	30	
Ser	Thr	Asp	Met	His	His	Ile	Glu	Glu	Ser	Phe	Gln	Glu	Ile	Lys	35	40	45	
Arg	Ala	Ile	Gln	Ala	Lys	Asp	Thr	Phe	Pro	Asn	Val	Thr	Ile	Leu	50	55	60	
Ser	Thr	Leu	Glu	Thr	Leu	Gln	Ile	Ile	Lys	Pro	Leu	Asp	Val	Cys	65	70	75	
Cys	Val	Thr	Lys	Asn	Leu	Leu	Ala	Phe	Tyr	Val	Asp	Arg	Val	Phe	80	85	90	
Lys	Asp	His	Gln	Glu	Pro	Asn	Pro	Lys	Ile	Leu	Arg	Lys	Ile	Ser	95	100	105	
Ser	Ile	Ala	Asn	Ser	Phe	Leu	Tyr	Met	Gln	Lys	Thr	Leu	Arg	Gln	110	115	120	
Cys	Gln	Glu	Gln	Arg	Gln	Cys	His	Cys	Arg	Gln	Glu	Ala	Thr	Asn	125	130	135	
Ala	Thr	Arg	Val	Ile	His	Asp	Asn	Tyr	Asp	Gln	Leu	Glu	Val	His	140	145	150	
Ala	Ala	Ala	Ile	Lys	Ser	Leu	Gly	Glu	Leu	Asp	Val	Phe	Leu	Ala				

155

160

165

Trp Ile Asn Lys Asn His Glu Val Met Phe Ser Ala  
170 175

<210> 510  
<211> 996  
<212> DNA  
<213> Homo Sapien

<400> 510  
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cacatacgat ttaggtgaca ctatagaata acatccactt tgcctttctc 150  
tccacaggtg tccactccca ggtccaactg cacctcgggt ctatcgataa 200  
tctcagcacc agccactcag agcagggcac gatgttgggg gcccgccctca 250  
ggctctgggt ctgtgccttg tgcagcgtct gcagcatgag cgtcctcaga 300  
gcctatccca atgcctcccc actgctcggc tccagctggg gtggcctgat 350  
ccacctgtac acagccacag ccaggaacag ctaccacctg cagatccaca 400  
agaatggcca tgtggatggc gcaccccatc agaccatcta cagtgccctg 450  
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cagaagatac ctctgcatgg atttcagagg caacattttt ggatcacact 550  
atttcgaccc ggagaactgc aggttccaac accagacgct ggaaaacggg 600  
tacgacgtct accactotcc tcagtatcac ttcttggtca gtctgggccg 650  
ggcgaagaga gccttcctgc caggcatgaa cccacccccg tactcccagt 700  
tcctgtcccg gaggaacgag atccccctaa ttcacttcaa ccccccata 750  
ccacggcggc acacccggag cgccgaggac gactcggagc gggaccccct 800  
gaacgtgctg aagccccggg cccggatgac cccggccccg gcctcctggt 850  
cacaggagct cccgagcgcc gaggacaaca gcccgatggc cagtgaacca 900  
ttaggggtgg tcagggggcg tcgagtgaac acgcacgctg ggggaacggg 950  
cccgaaggc tgccgcccct tcgccaagtt catctagggt cgctgg 996

<210> 511  
<211> 251  
<212> PRT  
<213> Homo Sapien

<400> 511  
Met Leu Gly Ala Arg Leu Arg Leu Trp Val Cys Ala Leu Cys Ser  
1 5 10 15  
Val Cys Ser Met Ser Val Leu Arg Ala Tyr Pro Asn Ala Ser Pro  
20 25 30

Leu	Leu	Gly	Ser	Ser	Trp	Gly	Gly	Leu	Ile	His	Leu	Tyr	Thr	Ala	
				35					40					45	
Thr	Ala	Arg	Asn	Ser	Tyr	His	Leu	Gln	Ile	His	Lys	Asn	Gly	His	
				50					55					60	
Val	Asp	Gly	Ala	Pro	His	Gln	Thr	Ile	Tyr	Ser	Ala	Leu	Met	Ile	
				65					70					75	
Arg	Ser	Glu	Asp	Ala	Gly	Phe	Val	Val	Ile	Thr	Gly	Val	Met	Ser	
				80					85					90	
Arg	Arg	Tyr	Leu	Cys	Met	Asp	Phe	Arg	Gly	Asn	Ile	Phe	Gly	Ser	
				95					100					105	
His	Tyr	Phe	Asp	Pro	Glu	Asn	Cys	Arg	Phe	Gln	His	Gln	Thr	Leu	
				110					115					120	
Glu	Asn	Gly	Tyr	Asp	Val	Tyr	His	Ser	Pro	Gln	Tyr	His	Phe	Leu	
				125					130					135	
Val	Ser	Leu	Gly	Arg	Ala	Lys	Arg	Ala	Phe	Leu	Pro	Gly	Met	Asn	
				140					145					150	
Pro	Pro	Pro	Tyr	Ser	Gln	Phe	Leu	Ser	Arg	Arg	Asn	Glu	Ile	Pro	
				155					160					165	
Leu	Ile	His	Phe	Asn	Thr	Pro	Ile	Pro	Arg	Arg	His	Thr	Arg	Ser	
				170					175					180	
Ala	Glu	Asp	Asp	Ser	Glu	Arg	Asp	Pro	Leu	Asn	Val	Leu	Lys	Pro	
				185					190					195	
Arg	Ala	Arg	Met	Thr	Pro	Ala	Pro	Ala	Ser	Cys	Ser	Gln	Glu	Leu	
				200					205					210	
Pro	Ser	Ala	Glu	Asp	Asn	Ser	Pro	Met	Ala	Ser	Asp	Pro	Leu	Gly	
				215					220					225	
Val	Val	Arg	Gly	Gly	Arg	Val	Asn	Thr	His	Ala	Gly	Gly	Thr	Gly	
				230					235					240	
Pro	Glu	Gly	Cys	Arg	Pro	Phe	Ala	Lys	Phe	Ile					
				245					250						

<210> 512  
 <211> 2015  
 <212> DNA  
 <213> Homo Sapien

<400> 512  
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 ctgctgggag gttgggggtct ctgggagctc tgcaggcccc agcaccgcga 150  
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 <211> 482  
 <212> PRT  
 <213> Homo Sapien

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                   20                  25                  30  
 Arg Ala Asp Thr Ala Met Thr Thr Asp Asp Thr Glu Val Pro Ala  
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 Met Thr Leu Ala Pro Gly His Ala Ala Leu Glu Thr Gln Thr Leu  
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 Ser Ala Glu Thr Ser Ser Arg Ala Ser Thr Pro Ala Gly Pro Ile  
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 Pro Glu Ala Glu Thr Arg Gly Ala Lys Arg Ile Ser Pro Ala Arg  
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 Glu Thr Arg Ser Phe Thr Lys Thr Ser Pro Asn Phe Met Val Leu  
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 Ile Ala Thr Ser Val Glu Thr Ser Ala Ala Ser Gly Ser Pro Glu  
                   110                  115                  120  
 Gly Ala Gly Met Thr Thr Val Gln Thr Ile Thr Gly Ser Asp Pro  
                   125                  130                  135  
 Glu Glu Ala Ile Phe Asp Thr Leu Cys Thr Asp Asp Ser Ser Glu  
                   140                  145                  150  
 Glu Ala Lys Thr Leu Thr Met Asp Ile Leu Thr Leu Ala His Thr  
                   155                  160                  165  
 Ser Thr Glu Ala Lys Gly Leu Ser Ser Glu Ser Ser Ala Ser Ser  
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 Asp Gly Pro His Pro Val Ile Thr Pro Ser Arg Ala Ser Glu Ser  
                   185                  190                  195  
 Ser Ala Ser Ser Asp Gly Pro His Pro Val Ile Thr Pro Ser Arg  
                   200                  205                  210  
 Ala Ser Glu Ser Ser Ala Ser Ser Asp Gly Pro His Pro Val Ile  
                   215                  220                  225  
 Thr Pro Ser Trp Ser Pro Gly Ser Asp Val Thr Leu Leu Ala Glu  
                   230                  235                  240  
 Ala Leu Val Thr Val Thr Asn Ile Glu Val Ile Asn Cys Ser Ile  
                   245                  250                  255

Thr Glu Ile Glu Thr Thr Thr Ser Ser Ile Pro Gly Ala Ser Asp	260	265	270
Ile Asp Leu Ile Pro Thr Glu Gly Val Lys Ala Ser Ser Thr Ser	275	280	285
Asp Pro Pro Ala Leu Pro Asp Ser Thr Glu Ala Lys Pro His Ile	290	295	300
Thr Glu Val Thr Ala Ser Ala Glu Thr Leu Ser Thr Ala Gly Thr	305	310	315
Thr Glu Ser Ala Ala Pro His Ala Thr Val Gly Thr Pro Leu Pro	320	325	330
Thr Asn Ser Ala Thr Glu Arg Glu Val Thr Ala Pro Gly Ala Thr	335	340	345
Thr Leu Ser Gly Ala Leu Val Thr Val Ser Arg Asn Pro Leu Glu	350	355	360
Glu Thr Ser Ala Leu Ser Val Glu Thr Pro Ser Tyr Val Lys Val	365	370	375
Ser Gly Ala Ala Pro Val Ser Ile Glu Ala Gly Ser Ala Val Gly	380	385	390
Lys Thr Thr Ser Phe Ala Gly Ser Ser Ala Ser Ser Tyr Ser Pro	395	400	405
Ser Glu Ala Ala Leu Lys Asn Phe Thr Pro Ser Glu Thr Pro Thr	410	415	420
Met Asp Ile Ala Thr Lys Gly Pro Phe Pro Thr Ser Arg Asp Pro	425	430	435
Leu Pro Ser Val Pro Pro Thr Thr Thr Asn Ser Ser Arg Gly Thr	440	445	450
Asn Ser Thr Leu Ala Lys Ile Thr Thr Ser Ala Lys Thr Thr Met	455	460	465
Lys Pro Gln Gln Pro Arg Pro Arg Leu Pro Gly Arg Gly Arg Pro	470	475	480

Gln Thr

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 <211> 2284  
 <212> DNA  
 <213> Homo Sapien

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 acccaactgc tacctatttt tctgtcccaa cgaggaagcc tgtccattga 550  
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<210> 515

<211> 431

<212> PRT

<213> Homo Sapien

<400> 515

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				20					25					30
Lys	Lys	Ser	Leu	Glu	Asp	Val	Val	Ile	Asp	Ile	Gln	Ser	Ser	Leu
				35					40					45
Ser	Lys	Gly	Ile	Arg	Gly	Asn	Glu	Pro	Val	Tyr	Thr	Ser	Thr	Gln
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Glu	Asp	Cys	Ile	Asn	Ser	Cys	Cys	Ser	Thr	Lys	Asn	Ile	Ser	Gly
				65					70					75
Asp	Lys	Ala	Cys	Asn	Leu	Met	Ile	Phe	Asp	Thr	Arg	Lys	Thr	Ala
				80					85					90
Arg	Gln	Pro	Asn	Cys	Tyr	Leu	Phe	Phe	Cys	Pro	Asn	Glu	Glu	Ala
				95					100					105
Cys	Pro	Leu	Lys	Pro	Ala	Lys	Gly	Leu	Met	Ser	Tyr	Arg	Ile	Ile
				110					115					120
Thr	Asp	Phe	Pro	Ser	Leu	Thr	Arg	Asn	Leu	Pro	Ser	Gln	Glu	Leu
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Pro	Gln	Glu	Asp	Ser	Leu	Leu	His	Gly	Gln	Phe	Ser	Gln	Ala	Val
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Thr	Pro	Leu	Ala	His	His	His	Thr	Asp	Tyr	Ser	Lys	Pro	Thr	Asp
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Ile	Ser	Trp	Arg	Asp	Thr	Leu	Ser	Gln	Lys	Phe	Gly	Ser	Ser	Asp
				170					175					180
His	Leu	Glu	Lys	Leu	Phe	Lys	Met	Asp	Glu	Ala	Ser	Ala	Gln	Leu
				185					190					195

Leu	Ala	Tyr	Lys	Glu 200	Lys	Gly	His	Ser	Gln 205	Ser	Ser	Gln	Phe	Ser 210
Ser	Asp	Gln	Glu	Ile 215	Ala	His	Leu	Leu	Pro 220	Glu	Asn	Val	Ser	Ala 225
Leu	Pro	Ala	Thr	Val 230	Ala	Val	Ala	Ser	Pro 235	His	Thr	Thr	Ser	Ala 240
Thr	Pro	Lys	Pro	Ala 245	Thr	Leu	Leu	Pro	Thr 250	Asn	Ala	Ser	Val	Thr 255
Pro	Ser	Gly	Thr	Ser 260	Gln	Pro	Gln	Leu	Ala 265	Thr	Thr	Ala	Pro	Pro 270
Val	Thr	Thr	Val	Thr 275	Ser	Gln	Pro	Pro	Thr 280	Thr	Leu	Ile	Ser	Thr 285
Val	Phe	Thr	Arg	Ala 290	Ala	Ala	Thr	Leu	Gln 295	Ala	Met	Ala	Thr	Thr 300
Ala	Val	Leu	Thr	Thr 305	Thr	Phe	Gln	Ala	Pro 310	Thr	Asp	Ser	Lys	Gly 315
Ser	Leu	Glu	Thr	Ile 320	Pro	Phe	Thr	Glu	Ile 325	Ser	Asn	Leu	Thr	Leu 330
Asn	Thr	Gly	Asn	Val 335	Tyr	Asn	Pro	Thr	Ala 340	Leu	Ser	Met	Ser	Asn 345
Val	Glu	Ser	Ser	Thr 350	Met	Asn	Lys	Thr	Ala 355	Ser	Trp	Glu	Gly	Arg 360
Glu	Ala	Ser	Pro	Gly 365	Ser	Ser	Ser	Gln	Gly 370	Ser	Val	Pro	Glu	Asn 375
Gln	Tyr	Gly	Leu	Pro 380	Phe	Glu	Lys	Trp	Leu 385	Leu	Ile	Gly	Ser	Leu 390
Leu	Phe	Gly	Val	Leu 395	Phe	Leu	Val	Ile	Gly 400	Leu	Val	Leu	Leu	Gly 405
Arg	Ile	Leu	Ser	Glu 410	Ser	Leu	Arg	Arg	Lys 415	Arg	Tyr	Ser	Arg	Leu 420
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<210> 516
<211> 2749
<212> DNA
<213> Homo Sapien
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<210> 517  
 <211> 332  
 <212> PRT  
 <213> Homo Sapien

<400> 517  
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 35 40 45  
 His Arg Lys Tyr Trp Cys Arg Lys Gly Gly Ile Leu Phe Ser Arg  
 50 55 60  
 Cys Ser Gly Thr Ile Tyr Ala Glu Glu Glu Gly Gln Glu Thr Met  
 65 70 75

Lys	Gly	Arg	Val	Ser	Ile	Arg	Asp	Ser	Arg	Gln	Glu	Leu	Ser	Leu	80	85	90
Ile	Val	Thr	Leu	Trp	Asn	Leu	Thr	Leu	Gln	Asp	Ala	Gly	Glu	Tyr	95	100	105
Trp	Cys	Gly	Val	Glu	Lys	Arg	Gly	Pro	Asp	Glu	Ser	Leu	Leu	Ile	110	115	120
Ser	Leu	Phe	Val	Phe	Pro	Gly	Pro	Cys	Cys	Pro	Pro	Ser	Pro	Ser	125	130	135
Pro	Thr	Phe	Gln	Pro	Leu	Ala	Thr	Thr	Arg	Leu	Gln	Pro	Lys	Ala	140	145	150
Lys	Ala	Gln	Gln	Thr	Gln	Pro	Pro	Gly	Leu	Thr	Ser	Pro	Gly	Leu	155	160	165
Tyr	Pro	Ala	Ala	Thr	Thr	Ala	Lys	Gln	Gly	Lys	Thr	Gly	Ala	Glu	170	175	180
Ala	Pro	Pro	Leu	Pro	Gly	Thr	Ser	Gln	Tyr	Gly	His	Glu	Arg	Thr	185	190	195
Ser	Gln	Tyr	Thr	Gly	Thr	Ser	Pro	His	Pro	Ala	Thr	Ser	Pro	Pro	200	205	210
Ala	Gly	Ser	Ser	Arg	Pro	Pro	Met	Gln	Leu	Asp	Ser	Thr	Ser	Ala	215	220	225
Glu	Asp	Thr	Ser	Pro	Ala	Leu	Ser	Ser	Gly	Ser	Ser	Lys	Pro	Arg	230	235	240
Val	Ser	Ile	Pro	Met	Val	Arg	Ile	Leu	Ala	Pro	Val	Leu	Val	Leu	245	250	255
Leu	Ser	Leu	Leu	Ser	Ala	Ala	Gly	Leu	Ile	Ala	Phe	Cys	Ser	His	260	265	270
Leu	Leu	Leu	Trp	Arg	Lys	Glu	Ala	Gln	Gln	Ala	Thr	Glu	Thr	Gln	275	280	285
Arg	Asn	Glu	Lys	Phe	Trp	Leu	Ser	Arg	Leu	Thr	Ala	Glu	Glu	Lys	290	295	300
Glu	Ala	Pro	Ser	Gln	Ala	Pro	Glu	Gly	Asp	Val	Ile	Ser	Met	Pro	305	310	315
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Ser Ala

<210> 518

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 518

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<210> 519

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 519

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<210> 520

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

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<210> 521

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 521

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<210> 522

<211> 24

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 522

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<210> 523

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<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

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<210> 524

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<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe  
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